

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 03:55:23 ; Search time 894 Seconds
(without alignments)
1335.249 Million cell updates/sec

Title: US-10-070-415a-37_COPY_410_430

Perfect score: 21
Sequence: 1 gcaagtgctgtagtgaggcg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sta.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_hlg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	581	6	BD178531 Method of
2	21	100.0	581	6	BD182924 Detection
3	20	95.2	581	6	BD178510 Method of
4	20	95.2	581	6	BD178511 Method of
5	20	95.2	581	6	BD178512 Method of
6	20	95.2	581	6	BD178513 Method of
7	20	95.2	581	6	BD182903 Detection
8	20	95.2	581	6	BD182904 Detection
9	20	95.2	581	6	BD182905 Detection
10	20	95.2	581	6	BD182906 Detection
11	19.4	92.4	581	6	BD090451 Carrier f
12	19.4	92.4	581	6	BD090452 Carrier f
13	19.4	92.4	581	6	BD090453 Carrier f
14	19.4	92.4	581	6	BD090454 Carrier f
15	19.4	92.4	581	6	BD090746 Polymorph
16	19.4	92.4	581	6	BD090747 Polymorph
17	19.4	92.4	581	6	BD090748 Polymorph
18	19.4	92.4	581	6	BD090749 Polymorph

M = A G C T

19	19.4	92.4	581	6	BD178532	Method of
20	19.4	92.4	581	6	BD178533	Method of
21	19.4	92.4	581	6	BD178534	Method of
22	19.4	92.4	581	6	BD182925	Detection
23	19.4	92.4	581	6	BD182926	Detection
24	19.4	92.4	581	6	BD182927	Detection
25	19.4	92.4	581	6	AR441761	Sequence
26	19.4	92.4	581	6	AR441762	Sequence
27	19.4	92.4	581	6	AR441763	Sequence
28	19.4	92.4	581	6	AR441764	Sequence
29	19.4	92.4	581	6	AR577621	Sequence
30	19.4	92.4	581	6	AR577622	Sequence
31	19.4	92.4	581	6	AR577623	Sequence
32	19.4	92.4	581	6	AR577624	Sequence
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39	19.4	92.4	108927	8	AP001609	Homo sapi
40	19.4	92.4	221285	14	AC023611	Mus muscu
41	19.4	92.4	340000	8	HS21C085	Homo sapi
42	18.4	87.6	69893	5	CR450734	Zebrafish
43	17.8	84.8	667	8	AY448313	Colobus g
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51	17.8	84.8	1047	5	AF076129	Scomberom
52	17.8	84.8	1047	5	AF076130	Scomberom
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76	17.4	81.0	599	8	D31907	Homo sapien
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78	17.4	81.0	2253	4	AY309439	Bos tauru
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91	16.8	80.0	633	6	AX622320	Sequence

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C 92 16.8 80.0 739 13 SVU27934 U27934 Stealth vir
 C 93 16.8 80.0 786 13 AF065677 AF065677 Stealth v
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 C 95 16.8 80.0 1030 5 AF186021 AF186021 Carassius
 C 96 16.8 80.0 1344 1 X78541 E.coli (O11
 C 97 16.8 80.0 1972 6 AR642915 Sequence
 C 98 16.8 80.0 1972 15 BT009556 Triticum
 C 99 16.8 80.0 2976 15 AY343340 Chlamydom
 C 100 16.8 80.0 4134 6 CS071660 Sequence

ALIGNMENTS

RESULT 1
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 DEFINITION Method of detecting nucleic acid relating to disease.
 ACCESSION BDI78531
 VERSION BDI78531.1 GI:30015797
 KEYWORDS WO 02077281-A/37.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 581)
 Hashimoto,K., Hashimoto,M., Mishirot,S. and Ota,Y.
 Method of detecting nucleic acid relating to disease
 Patent: WO 02077281-A 37 03-OCT-2002;
 JOURNAL TOSHIBA CORP,KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,
 YASUHIKO OTA
 OS Homo sapiens (human)
 PN WO 02077281-A/37
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12Q1/68,C12N15/09,C12M1/00,G01N33/53,G01N33/566, PC
 G01N33/576,
 PC G01N37/00
 CC Method of detecting nucleic acid relating to disease FH Key
 FT source 1..581
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 OS Homo sapiens (human)
 PN WO 02077281-A/37
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
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 PN WO 02077281-A/37
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12Q1/68,C12N15/09,C12M1/00,G01N33/53,G01N33/566, PC
 G01N33/576,
 PC G01N37/00
 CC Method of detecting nucleic acid relating to disease FH Key
 FT source 1..581
 FT Location/Qualifiers
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 DEFINITION Detection of nucleic acid associated with disease.
 ACCESSION BDI82924
 VERSION BDI82924.1 GI:31875124
 KEYWORDS JP 200235083-A/37.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 581)
 AUTHORS Hashimoto,K., Hashimoto,M., Mishirot,S. and Ota,Y.
 TITLE Detection of nucleic acid associated with disease
 JOURNAL Patent: JP 200235083-A 37 10-DEC-2002;
 COMMENT TOSHIBA CORP
 OS Homo sapiens (human)
 PN JP 200235083-A/37
 PD 10-DEC-2002
 PF 26-MAR-2002 JP 2002086681
 PI KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
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 PC G01N33/576/(C12Q1/68,C12R1:93),C12N15/00,C12N15/00 CC
 Detection of nucleic acid associated with disease FH Key
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 OS Homo sapiens (human)
 PN WO 02077281-A/16
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12Q1/68,C12N15/09,C12M1/00,G01N33/53,G01N33/566, PC
 G01N33/576,
 PC G01N37/00
 CC Method of detecting nucleic acid relating to disease FH Key
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 DEFINITION Method of detecting nucleic acid relating to disease.
 ACCESSION BDI78510
 VERSION BDI78510.1 GI:30015776
 KEYWORDS WO 02077281-A/16.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 581)
 Hashimoto,K., Hashimoto,M., Mishirot,S. and Ota,Y.
 Method of detecting nucleic acid relating to disease
 Patent: WO 02077281-A 16 03-OCT-2002;
 JOURNAL TOSHIBA CORP,KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,
 YASUHIKO OTA
 OS Homo sapiens (human)
 PN WO 02077281-A/16
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12Q1/68,C12N15/09,C12M1/00,G01N33/53,G01N33/566, PC
 G01N33/576,
 PC G01N37/00
 CC Method of detecting nucleic acid relating to disease FH Key
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 PN WO 02077281-A/16
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12Q1/68,C12N15/09,C12M1/00,G01N33/53,G01N33/566, PC
 G01N33/576,
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 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
 C12Q1/68,C12N15/09,C12M1/00,G01N33/53,G01N33/566, PC
 G01N33/576,
 PC G01N37/00
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD178511 581 bp DNA linear PAT 16-APR-2003
Method of detecting nucleic acid relating to disease.
BD178511
BD178511.1 GI:30015777
WO 02077281-A/17.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Method of detecting nucleic acid relating to disease
Patent: WO 02077281-A 17 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
OS Homo sapiens (human)
PN WO 02077281-A/17
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
G01N33/576,
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key

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Best Local Similarity 95.2%; Pred. No. 41;
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RESULT 5
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD178512 581 bp DNA linear PAT 16-APR-2003
Method of detecting nucleic acid relating to disease.
BD178512
BD178512.1 GI:30015778
WO 02077281-A/18.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Method of detecting nucleic acid relating to disease
Patent: WO 02077281-A 18 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
OS Homo sapiens (human)
PN WO 02077281-A/18
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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CC Method of detecting nucleic acid relating to disease FH Key

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Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGGTGCGGG 21
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410 GCAAGTCTGNAGGTGCGGG 430

RESULT 6
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD178513 581 bp DNA linear PAT 16-APR-2003
Method of detecting nucleic acid relating to disease.
BD178513
BD178513.1 GI:30015779
WO 02077281-A/19.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Method of detecting nucleic acid relating to disease
Patent: WO 02077281-A 19 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
OS Homo sapiens (human)
PN WO 02077281-A/19
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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CC Method of detecting nucleic acid relating to disease FH Key

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Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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PD 03-OCT-2002
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C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGGTGCGGG 21
|||||
410 GCAAGTCTGNAGGTGCGGG 430

RESULT 6
BD178513
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD178513 581 bp DNA linear PAT 16-APR-2003
Method of detecting nucleic acid relating to disease.
BD178513
BD178513.1 GI:30015779
WO 02077281-A/19.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Method of detecting nucleic acid relating to disease
Patent: WO 02077281-A 19 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
OS Homo sapiens (human)
PN WO 02077281-A/19
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
G01N33/576,
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key

FT source 1.581
Location/Qualifiers
/organism="Homo sapiens (human)"

FEATURES
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1.581
Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN
Query Match 95.2%; Score 20; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGGTGCGGG 21
|||||
410 GCAAGTCTGNAGGTGCGGG 430

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RESULT 7
BD182903
LOCUS      BD182903          581 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182903
VERSION    BD182903.1 GI:31875103
KEYWORDS   JP 2002355083-A/16.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 16 10-DEC-2002;
TOSHIBA CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002355083-A/16
            PD 10-DEC-2002
            PF 26-MAR-2002 JP 2002086681
            PI KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,PC
            G01N33/569,
            PC G01N33/576/(C12Q1/68,C12R1/93),C12N15/00,C12N15/00 CC
            Detection of nucleic acid associated with disease FH Key
            Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN
Query Match      95.2%; Score 20; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGTGGCGGG 21
        ||||||| |||||||
Db      410 GCAAGTGCTGNAGTGGCGGG 430

RESULT 8
BD182904
LOCUS      BD182904          581 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182904
VERSION    BD182904.1 GI:31875104
KEYWORDS   JP 2002355083-A/17.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 17 10-DEC-2002;
TOSHIBA CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002355083-A/17
            PD 10-DEC-2002
            PF 26-MAR-2002 JP 2002086681
            PI KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,PC
            G01N33/569,
            PC G01N33/576/(C12Q1/68,C12R1/93),C12N15/00,C12N15/00 CC
            Detection of nucleic acid associated with disease FH Key
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            FT /organism='Homo sapiens (human)'.

FEATURES             Location/Qualifiers
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ORIGIN
Query Match      95.2%; Score 20; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGTGGCGGG 21
        ||||||| |||||||
Db      410 GCAAGTGCTGNAGTGGCGGG 430

RESULT 9
BD182905
LOCUS      BD182905          581 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182905
VERSION    BD182905.1 GI:31875105
KEYWORDS   JP 2002355083-A/18.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 18 10-DEC-2002;
TOSHIBA CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002355083-A/18
            PD 10-DEC-2002
            PF 26-MAR-2002 JP 2002086681
            PI KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,PC
            G01N33/569,
            PC G01N33/576/(C12Q1/68,C12R1/93),C12N15/00,C12N15/00 CC
            Detection of nucleic acid associated with disease FH Key
            Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

ORIGIN
Query Match      95.2%; Score 20; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGTGGCGGG 21
        ||||||| |||||||
Db      410 GCAAGTGCTGNAGTGGCGGG 430

RESULT 10
BD182906
LOCUS      BD182906          581 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182906
VERSION    BD182906.1 GI:31875106
KEYWORDS   JP 2002355083-A/19.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 19 10-DEC-2002;
TOSHIBA CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002355083-A/19
            PD 10-DEC-2002
            PF 26-MAR-2002 JP 2002086681
            PI KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,PC
            G01N33/569,
            PC G01N33/576/(C12Q1/68,C12R1/93),C12N15/00,C12N15/00 CC
            Detection of nucleic acid associated with disease FH Key
            Location/Qualifiers
            FT source 1..581
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FEATURES             Location/Qualifiers
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ORIGIN
Query Match      95.2%; Score 20; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGTGGCGGG 21
        ||||||| |||||||
Db      410 GCAAGTGCTGNAGTGGCGGG 430
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease
Patent: JP 200235083-A 19 10-DEC-2002;
TOSHIBA CORP
OS Homo sapiens (human)
PN JP 200235083-A/19
PD 10-DEC-2002
PF 26-MAR-2002 JP 2002086681
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
G01N33/569,
PC G01N33/576/(C12Q1/68, C12R1/93), C12N15/00, C12N15/00 CC
Detection of nucleic acid associated with disease FH Key
Location/Qualifiers
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FT Location/Qualifiers
1..581
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Query Match 95.2%; Score 20; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTGTAGTGGCGGG 21
|||||
DB 410 GCAAGTGTGTAGTGGCGGG 430
RESULT 11
BD090451
LOCUS
DEFINITION
Carrier for detecting gene, and its use for detecting efficacy of
interferon therapy.
ACCESSION
BD090451.1 GI:22636061
VERSION
JP 2001333786-A/1.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.
Carrier for detecting gene, and its use for detecting efficacy of
interferon therapy
Patent: JP 2001333786-A 1 04-DEC-2001;
TOSHIBA CORP
OS Homo sapiens (human)
PN JP 2001333786-A/1
PD 04-DEC-2001
PF 06-MAR-2001 JP 2001062372
PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI
HASHIMOTO
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00
CC Carrier for detecting gene, and its use
for detecting efficacy
of
CC interferon therapy
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.
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1..581
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
ORIGIN
Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTGTAGTGGCGGG 21
|||||
DB 410 GCAAGTGTGTAGTGGCGGG 430
RESULT 13
BD090453.
LOCUS
DEFINITION
Carrier for detecting gene, and its use for detecting efficacy of
interferon therapy.
ACCESSION
BD090453.1 GI:22636063
KEYWORDS
JP 2001333786-A/3.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Hashimoto, M., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease
Patent: JP 200235083-A 19 10-DEC-2002;
TOSHIBA CORP
OS Homo sapiens (human)
PN JP 200235083-A/19
PD 10-DEC-2002
PF 26-MAR-2002 JP 2002086681
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
G01N33/569,
PC G01N33/576/(C12Q1/68, C12R1/93), C12N15/00, C12N15/00 CC
Detection of nucleic acid associated with disease FH Key
Location/Qualifiers
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Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTGTAGTGGCGGG 21
|||||
DB 410 GCAAGTGTGTAGTGGCGGG 430
RESULT 13
BD090453.
LOCUS
DEFINITION
Carrier for detecting gene, and its use for detecting efficacy of
interferon therapy.
ACCESSION
BD090453.1 GI:22636063
KEYWORDS
JP 2001333786-A/3.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 581)
 AUTHORS Tsuchikata,M., Mishiro,T., Ota,H. and Hashimoto,K.
 TITLE Carrier for detecting gene, and its use for detecting efficacy of
 interferon therapy
 JOURNAL Patent: JP 2001333786-A 3 04-DEC-2001;
 TOSHIBA CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2001333786-A/3
 PD 04-DEC-2001
 PF 06-MAR-2001 JP 2001062372
 PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI
 HASHIMOTO
 PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC
 G01N37/00,
 CC C12N15/00
 CC Carrier for detecting gene, and its use
 for detecting efficacy
 CC
 CC interferon therapy
 FH key Location/Qualifiers
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 Best Local Similarity 95.2%; Pred. No. 83;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTGCTGTAGTGGGG 21
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 Db 410 GCAAGTGCTGTAGTGGGG 430
 |||||
 RESULT 14
 BD090454 581 bp DNA linear PAT 27-AUG-2002
 LOCUS
 DEFINITION Carrier for detecting gene, and its use for detecting efficacy of
 interferon therapy.
 ACCESSION BD090454
 VERSION BD090454.1 GI:22636064
 KEYWORDS JP 2001333786-A/4.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 581)
 AUTHORS Tsuchikata,M., Mishiro,T., Ota,H. and Hashimoto,K.
 TITLE Carrier for detecting gene, and its use for detecting efficacy of
 interferon therapy
 JOURNAL Patent: JP 2001333786-A 4 04-DEC-2001;
 TOSHIBA CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2001333786-A/4
 PD 04-DEC-2001
 PF 06-MAR-2001 JP 2001062372
 PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI
 HASHIMOTO
 PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC
 G01N37/00,
 CC C12N15/00
 CC Carrier for detecting gene, and its use
 for detecting efficacy

CC of
 CC interferon therapy
 FH key Location/Qualifiers
 FT source 1..581
 FT /organism='Homo sapiens (human)'
 FT /mol_type='genomic DNA'
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 Best Local Similarity 95.2%; Pred. No. 83;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTGCTGTAGTGGGG 21
 |||||
 Db 410 GCAAGTGCTGTAGTGGGG 430
 |||||
 RESULT 15
 BD090746 581 bp DNA linear PAT 27-AUG-2002
 LOCUS
 DEFINITION Polymorphic gene of MxA protein and use thereof.
 ACCESSION BD090746
 VERSION BD090746.1 GI:22636356
 KEYWORDS JP 2001333785-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 581)
 AUTHORS Tsuchikata,M., Mishiro,T., Ota,H. and Hashimoto,K.
 TITLE Polymorphic gene of MxA protein and use thereof
 JOURNAL Patent: JP 2001333785-A 1 04-DEC-2001;
 TOSHIBA CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2001333785-A/1
 PD 04-DEC-2001
 PF 06-MAR-2001 JP 2001062371
 PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI
 HASHIMOTO
 PC C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61K48/00, A61P15/00, PC
 A61P25/00,
 PC A61P27/02, A61P27/16, A61P31/12, A61P31/20, A61P31/22, A61P35/00,
 PC A61P35/02,
 PC A61P43/00, C12N5/10, C12Q1/68, C12Q1/70, C12N15/00, C12N5/
 PC 00
 CC Polymorphic gene of MxA protein and use thereof FH Key
 CC Location/Qualifiers
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 FT /mol_type='genomic DNA'
 FT /db_xref='taxon:9606'
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 Location/Qualifiers
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 Query Match 92.4%; Score 19.4; DB 6; Length 581;
 Best Local Similarity 95.2%; Pred. No. 83;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTGCTGTAGTGGGG 21
 |||||
 Db 410 GCAAGTGCTGTAGTGGGG 430
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 RESULT 16
 BD090747

LOCUS	BD090747	581 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Polymorphic gene of MxA protein and use thereof.				
ACCESSION	BD090747				
VERSION	BD090747.1	GI:22636357			
KEYWORDS	JP 2001333785-A/2.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.				
TITLE	Polymorphic gene of MxA protein and use thereof				
JOURNAL	Patent: JP 2001333785-A 2 04-DEC-2001;				
COMMENT	TOSHIBA CORP				
	OS	Homo sapiens (human)			
	PN	JP 2001333785-A/2			
	PD	04-DEC-2001			
	PF	06-MAR-2001	JP 2001062371		
	PI	MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI			
	PC	HASHIMOTO			
	C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61K48/00, A61P15/00, PC				
	A61P27/02, A61P27/16, A61P31/12, A61P31/20, A61P31/22, A61P35/00, PC				
	A61P35/02, A61P43/00, C12N5/10, C12Q1/68, C12Q1/70, C12N15/00, C12N5/00				
	CC	Polymorphic gene of MxA protein and use thereof	Key		
	Location/Qualifiers				
FT	source	1..581			
FT	Location/Qualifiers	/organism="Homo sapiens (human)"			
FEATURES	source	1..581			
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		/db_xref="taxon:9606"			
ORIGIN					
Query Match	92.4%;	Score 19.4;	DB 6;	Length 581;	
Best Local Similarity	95.2%;	Pred. No. 83;			
Matches	20; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
QY	1	GCAAGTGCTGTAGTGGGGG 21			
DB	410	GCAAGTGCTGAGGTGGGGG 430			
RESULT 17					
BD090748					
LOCUS	BD090748	581 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Polymorphic gene of MxA protein and use thereof.				
ACCESSION	BD090748				
VERSION	BD090748.1	GI:22636358			
KEYWORDS	JP 2001333785-A/3.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.				
TITLE	Polymorphic gene of MxA protein and use thereof				
JOURNAL	Patent: JP 2001333785-A 3 04-DEC-2001;				
COMMENT	TOSHIBA CORP				
	OS	Homo sapiens (human)			
	PN	JP 2001333785-A/3			
	PD	04-DEC-2001			
	PF	06-MAR-2001	JP 2001062371		
	PI	MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI			
	PC	HASHIMOTO			
	C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61K48/00, A61P15/00, PC				

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RESULT 19
BD178532
LOCUS BD178532 581 bp DNA linear PAT 16-APR-2003
DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178532
VERSION BD178532.1 GI:30015798
KEYWORDS WO 02077281-A/38.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Hashimoto K., Hashimoto M., Mishiro S. and Ota Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 38 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
PN WO 02077281-A/38
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C1201/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
G01N33/576
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key
FT source
FT 1. .581
Location/Qualifiers
/organism="Homo sapiens (human)"
/db_xref="taxon:9606"
FEATURES
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Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGAGGTGCGGG 430
|||||

RESULT 20
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LOCUS BD178533 581 bp DNA linear PAT 16-APR-2003
DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178533
VERSION BD178533.1 GI:30015799
KEYWORDS WO 02077281-A/39.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Hashimoto K., Hashimoto M., Mishiro S. and Ota Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 39 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
PN WO 02077281-A/39
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C1201/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
G01N33/576
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key
FT source
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/db_xref="taxon:9606"
FEATURES
source
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Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGCTGTAGTGGCGGG 21
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Db 410 GCAAGTGCTGAGGTGCGGG 430
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C1201/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
G01N33/576,
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key
FT source
FT 1. .581
Location/Qualifiers
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/db_xref="taxon:9606"
FEATURES
source
ORIGIN
Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGAGGTGCGGG 430
|||||

RESULT 21
BD178534
LOCUS BD178534 581 bp DNA linear PAT 16-APR-2003
DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178534
VERSION BD178534.1 GI:30015800
KEYWORDS WO 02077281-A/40.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Hashimoto K., Hashimoto M., Mishiro S. and Ota Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 40 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
PN WO 02077281-A/40
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C1201/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
G01N33/576
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key
FT source
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Location/Qualifiers
/organism="Homo sapiens (human)"
/db_xref="taxon:9606"
FEATURES
source
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Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGAGGTGCGGG 430
|||||

RESULT 22
BD182925
LOCUS BD182925 581 bp DNA linear PAT 17-JUN-2003

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DEFINITION Detection of nucleic acid associated with disease.

BD182925

ACCESSION BD182925.1 GI:31875125

VERSION JP 2002355083-A/38.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease

PATENT: JP 2002355083-A 38 10-DEC-2002;

TOSHIBA CORP

OS Homo sapiens (human)

PN JP 2002355083-A/38

PD 10-DEC-2002

PP 26-MAR-2002 JP 2002086681

PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC

GO1N33/569,

PC GO1N33/576/(C12Q1/68, C12R1:93), C12N15/00, C12N15/00 CC

Detection of nucleic acid associated with disease FH Key

FT Location/Qualifiers

FT source 1..581

Location/Qualifiers

/organism='Homo sapiens (human)'

1..581

/mol_type='genomic DNA'

/db_xref='taxon:9606'

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;

Best Local Similarity 95.2%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21

DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 23

BD182926

LOCUS 581 bp DNA linear PAT 17-JUN-2003

DEFINITION Detection of nucleic acid associated with disease.

BD182926

ACCESSION BD182926.1 GI:31875126

VERSION JP 2002355083-A/39.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease

PATENT: JP 2002355083-A 39 10-DEC-2002;

TOSHIBA CORP

OS Homo sapiens (human)

PN JP 2002355083-A/39

PD 10-DEC-2002

PP 26-MAR-2002 JP 2002086681

PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC

GO1N33/569,

PC GO1N33/576/(C12Q1/68, C12R1:93), C12N15/00, C12N15/00 CC

Detection of nucleic acid associated with disease FH Key

FT Location/Qualifiers

FT source 1..581

Location/Qualifiers

/organism='Homo sapiens (human)'

1..581

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;

Best Local Similarity 95.2%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21

DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 25

BD182927

LOCUS 581 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 1 from patent US 6667155.

BD182927

ACCESSION BD182927.1 GI:42667980

VERSION

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM

Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease

PATENT: JP 2002355083-A 40 10-DEC-2002;

TOSHIBA CORP

OS Homo sapiens (human)

PN JP 2002355083-A/40

PD 10-DEC-2002

PP 26-MAR-2002 JP 2002086681

PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;

Best Local Similarity 95.2%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21

DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 24

BD182927

LOCUS 581 bp DNA linear PAT 17-JUN-2003

DEFINITION Detection of nucleic acid associated with disease.

BD182927

ACCESSION BD182927.1 GI:31875127

VERSION JP 2002355083-A/40.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 581)

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;

Best Local Similarity 95.2%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21

DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 25

BD182927

LOCUS 581 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 1 from patent US 6667155.

BD182927

ACCESSION BD182927.1 GI:42667980

VERSION

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM

Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease

PATENT: JP 2002355083-A 40 10-DEC-2002;

TOSHIBA CORP

OS Homo sapiens (human)

PN JP 2002355083-A/40

PD 10-DEC-2002

PP 26-MAR-2002 JP 2002086681

PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC

GO1N33/569,

PC GO1N33/576/(C12Q1/68, C12R1:93), C12N15/00, C12N15/00 CC

Detection of nucleic acid associated with disease FH Key

FT Location/Qualifiers

FT source 1..581

Location/Qualifiers

/organism='Homo sapiens (human)'

1..581

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;

Best Local Similarity 95.2%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21

DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 25

BD182927

LOCUS 581 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 1 from patent US 6667155.

BD182927

ACCESSION BD182927.1 GI:42667980

VERSION

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM

Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease

PATENT: JP 2002355083-A 40 10-DEC-2002;

TOSHIBA CORP

OS Homo sapiens (human)

PN JP 2002355083-A/40

PD 10-DEC-2002

PP 26-MAR-2002 JP 2002086681

PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC

JOURNAL Patent: US 6667155-A 1 23-DEC-2003;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;

FEATURES
source Location/Qualifiers
1. .581
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 26
AR441762
LOCUS AR441762 581 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2 from patent US 6667155.
ACCESSION AR441762
VERSION AR441762.1 GI:42667981
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.
TITLE Carrier for gene detection and its use for detecting validity of
interferon therapy
JOURNAL Patent: US 6667155-A 2 23-DEC-2003;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;

FEATURES
source Location/Qualifiers
1. .581
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/mol_type="genomic DNA"

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 27
AR441763
LOCUS AR441763 581 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6667155.
ACCESSION AR441763
VERSION AR441763.1 GI:42667982
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.
TITLE Carrier for gene detection and its use for detecting validity of
interferon therapy
JOURNAL Patent: US 6667155-A 3 23-DEC-2003;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;

FEATURES
source Location/Qualifiers
1. .581
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 28
AR441764
LOCUS AR441764 581 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 4 from patent US 6667155.
ACCESSION AR441764
VERSION AR441764.1 GI:42667983
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.
TITLE Carrier for gene detection and its use for detecting validity of
interferon therapy
JOURNAL Patent: US 6667155-A 4 23-DEC-2003;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 29
AR577621
LOCUS AR577621 581 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 1 from patent US 6783935.
ACCESSION AR577621
VERSION AR577621.1 GI:56580247
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.
TITLE Genetic polymorphism of MxA protein and use thereof
JOURNAL Patent: US 6783935-A 1 31-AUG-2004;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 30

AR577622
LOCUS AR577622 581 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 2 from patent US 6783935.
ACCESSION AR577622
VERSION AR577622.1 GI:56580248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata, M., Mishiro, S., Oota, Y. and Hashimoto, K.
TITLE Genetic polymorphism of MxA protein and use thereof
JOURNAL Patent: US 6783935-A 2 31-AUG-2004;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;
FEATURES
source Location/Qualifiers
1..581
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430
RESULT 31
LOCUS AR577623 581 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 3 from patent US 6783935.
ACCESSION AR577623
VERSION AR577623.1 GI:56580249
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata, M., Mishiro, S., Oota, Y. and Hashimoto, K.
TITLE Genetic polymorphism of MxA protein and use thereof
JOURNAL Patent: US 6783935-A 3 31-AUG-2004;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;
FEATURES
source Location/Qualifiers
1..581
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430
RESULT 32
LOCUS AR577624 581 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 4 from patent US 6783935.
ACCESSION AR577624
VERSION AR577624.1 GI:56580250
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 581)
AUTHORS Hijikata, M., Mishiro, S., Oota, Y. and Hashimoto, K.

Genetic polymorphism of MxA protein and use thereof
Patent: US 6783935-A 4 31-AUG-2004;
Kabushiki Kaisha Toshiba; Kawasaki;
JPX;
FEATURES
source Location/Qualifiers
1..581
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430
RESULT 33
LOCUS HSMXAP 1899 bp DNA linear PRI 09-SEP-2004
DEFINITION H.sapiens DNA for MxA promoter.
ACCESSION X55639
VERSION X55639.1 GI:456344
KEYWORDS MxA promoter.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Chang, K.C., Hansen, E., Foroni, L., Lida, J. and Goldspink, G.
TITLE Molecular and functional analysis of the virus- and
interferon-inducible human MxA promoter
JOURNAL Arch. Virol. 117 (1-2), 1-15 (1991)
PUBMED 1706589
REFERENCE 2 (bases 1 to 1899)
AUTHORS Chang, K.C.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1990) Chang K.-C., The Royal Veterinary College,
University of London, Royal College Street, London NW1 0TU, U K
FEATURES
source Location/Qualifiers
1..1899
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/cell_line="COLO 320"
/tissue_type="tumour"
115..128
/note="ISRE"
promoter
514..525
/note="ISRE"
promoter
559..570
/note="ISRE"
promoter
581..589
/note="GC box"
exon
616..652
/number=1
exon
1583..1681
/number=2
ORIGIN
Query Match 92.4%; Score 19.4; DB 8; Length 1899;
Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 483 GCAAGTGTCTAGGTGCGGG 503

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RESULT 34
HUM8DC6Z/c
LOCUS
DEFINITION Homo sapiens (subclone H8 4_b9 from P1 35 H5 C8) DNA linear PRI 22-AUG-1994
ACCESSION L35661.1 GI:532026
VERSION MX1 region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 3339)
Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A.,
Ericsson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M.,
Mayeda,C.A., Steiert-El Khair,A. and Palazzolo,M.J.
Sequencing of the MX1 region on human chromosome 21
Unpublished (1994)
ORIGINAL SOURCE text: Homo sapiens (library: Subclones in pSP72
from P1 clone 35 H5 C8 (H8)) DNA.
Sequence submitted by:
Human Genome Center and
Drosophila Genome Center
Lawrence Berkeley Laboratory
Berkeley, CA 94720
e-mail: seq@genome.lbl.gov
This subclone overlaps H8 6_e2 and H8 3_d9.
FEATURES
source
1..3339
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_lib="Subclones in pSP72 from P1 clone 35 H5 C8
(H8)"
ORIGIN
Query Match 92.4%; Score 19.4; DB 8; Length 3339;
Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGCGGG 21
Db 2664 GCAAGTCTGCAGGTGGCGGG 2644

RESULT 35
CS124352
LOCUS
DEFINITION Sequence 38 from Patent WO2005059172.
ACCESSION CS124352
VERSION CS124352.1 GI:71057417
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Fockens,J.
METHOD and nucleic acids for the improved treatment of breast cell
proliferative disorders
Patent: WO 2005059172-A 38 30-JUN-2005;
JOURNAL Epigenomics AG (DE)
FEATURES
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Query Match 92.4%; Score 19.4; DB 6; Length 4341;
Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GCAAGTCTGTAGTGGCGGG 21
Db 1557 GCAAGTCTGCAGGTGGCGGG 1577

RESULT 36
HS25D2
LOCUS
DEFINITION Homo sapiens chromosome 21 from cosmid LL21NC02-25D2 map
21q22.2,D21S349-MX1, complete sequence.
ACCESSION AL773576 AJ011929 AL442167
VERSION AL773576.1 GI:21538700
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Ramser,J., Francis,F., Beck,A., Hennig,S., Klages,S., Borzym,K.,
Langer,I., Steffens,C., Hildmann,T., Dagand,E., Yaspo,M.,
Reinhardt,R. and Lehrach,H.
Unpublished
2 (bases 1 to 40100)
MPIMG.
Direct Submission
Submitted (01-OCT-1998) MPIMG, Abt. Lehrach, Max Planck Institut
fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195, Germany
Clones received from Resource Centre of the Human Genome Project at
the Max-Planck-Institut for Molecular Genetics.
This submission was part of AL442167 and AJ011929
Mapping info:
AL442166 1..300050
AL442167 1..313064
AL773569 (PAC RPCI-1 247E2)
AL773573 (PAC RPCI-1 146B4)
AL773572 (PAC RPCI-1 141D16)
AL773575 (PAC RPCI-1 269A14)
AL773570 (cosmid LLNLC116 44C5)
AL773578 (PAC RPCI-1 265B9)
AL773574 (cosmid LLNLC116 16H18)
AL773577 (cosmid LLNLC116 14C10)
AL773576 (cosmid LLNLC116 25D2)
AL773571 (cosmid LLNLC116 87D5)
AJ011929 592889..594336, cosmid LLNLC116 87D5 22828..24275 sequence
from clone KB447A5, accession no. AP001609 (DDBJ), sequenced at
KEIO university, Tokyo, Japan.
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/chromosome="21"
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/clone="LL21NC02-25D2"
/library, Lawrence Livermore National Laboratory (LLNL),
creator: Pieter de Jong; PAC: RPCI1,3-5, Roswell Park
Cancer Institute, creator: Pieter de Jong, P.Ioannou"
ORIGIN
Query Match 92.4%; Score 19.4; DB 8; Length 40100;
Best Local Similarity 95.2%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGCGGG 21
Db 6042 GCAAGTCTGCAGGTGGCGGG 6062

RESULT 37
HS14C10
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LOCUS      HS14C10                      41120 bp      DNA      linear      PRI 06-MAY-2003
DEFINITION Homo sapiens chromosome 21 from cosmid LL21NC02-14C10 map
ACCESSION  21q22.2,D21S349-MX1, complete sequence.
VERSION    AL773577 AJ011929 AL442167
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE  1
AUTHORS    Ramser,J., Francis,F., Beck,A., Hennig,S., Klages,S., Borzym,K.,
            Reinhardt,R. and Lehrach,H.
JOURNAL    Unpublished
TITLE      2 (bases 1 to 41120)
AUTHORS     MPING.
JOURNAL    Direct Submission
COMMENT    Submitted (01-OCT-1998) MPING, Abt. Lehrach, Max Planck Institut
            fuer Molekulare Genetik, Innestrasse 73, Berlin, 14195, Germany
            Clones received from Resource Centre of the Human Genome Project at
            the Max-Planck-Institut for Molecular Genetics
            This submission was part of AL442167 and AJ011929
            Mapping info:
            AL442166 1..300050      <=> AJ011929 1..300050
            AL442167 1..313064      <=> AJ011929 300000..613064
            AL773569 (PAC RPCI-1 247E2) <=> AJ011929 1..153758
            AL773573 (PAC RPCI-1 146B4) <=> AJ011929 138212..246050
            AL773572 (PAC RPCI-1 141D16) <=> AJ011929 211573..357649
            AL773575 (PAC RPCI-1 269A14) <=> AJ011929 296228..392080
            AL773570 (cosmid LLNLC116 44C5) <=> AJ011929 362796..408363
            AL773578 (PAC RPCI-1 265B9) <=> AJ011929 384408..542081
            AL773574 (cosmid LLNLC116 16H18) <=> AJ011929 439926..475647
            AL773577 (cosmid LLNLC116 14C10) <=> AJ011929 514758..555921
            AL773576 (cosmid LLNLC116 25D2) <=> AJ011929 538954..579053
            AL773571 (cosmid LLNLC116 87D5) <=> AJ011929 570062..613064
            AJ011929 592889..594336, cosmid LLNLC116 87D5 22828..24275 sequence
            from clone KB447A5, accession no. AP001609 (DDBJ), sequenced at
            KEIO university, Tokyo, Japan.

FEATURES             Location/Qualifiers
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                     /clone="LL21NC02-14C10"
                     library="Lawrence Livermore National Laboratory (LLNL)",
                     creator: Pieter de Jong; PAC: RPCI1,3-5, Roswell Park
                     Cancer Institute, creator: Pieter de Jong, P.Ioannou"

ORIGIN
Query Match      92.4%; Score 19.4; DB 8; Length 41120;
Best Local Similarity 95.2%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTGTCTAGGTGCGGGG 21
      |||||
DB  30194 GCAAGTGTCTAGGTGCGGGG 30214

RESULT 38
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LOCUS      AC005612                      60904 bp      DNA      linear      PRI 04-SEP-1998
DEFINITION Homo sapiens chromosome 21, P1 clone LBL#8 (LENL H8), complete
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ACCESSION  AC005612
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE  1
AUTHORS    Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
JOURNAL    Unpublished
TITLE      2 (bases 1 to 60904)
AUTHORS     Riche,D.O.
JOURNAL    Large Scale Sequence Analysis and Annotation with the Sequence
            Comparison Analysis (SCAN) System
            Unpublished
            3 (bases 1 to 60904)
AUTHORS     Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
JOURNAL    Direct Submission
COMMENT    Submitted (04-SEP-1998) Human Genome Center, DOE Joint Genome
            Institute, Lawrence Berkeley National Laboratory, MS 74-157,
            Berkeley, CA 94720, U.S.A.
            Sequence submitted by:
            DOE Joint Genome Institute.
            Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 60904)

AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 60904)

AUTHORS Riche,D.O.

JOURNAL Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System

REFERENCE 3 (bases 1 to 60904)

AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.

JOURNAL Direct Submission

COMMENT Submitted (04-SEP-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.

Sequence submitted by:

DOE Joint Genome Institute.

FEATURES

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complement(13974..14029)

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15399..15473

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/note="GRAIL 2 excellent exon, frame 0"

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repeat_region	/rpt family="Alu"	43942. .44219	
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repeat_region	/rpt family="Alu"	complement(46007. .46178)	
misc_feature	20241. .20286	/rpt family="Alu"	
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repeat_region	21081. .21263	/note="GRAIL 2 excellent exon, frame 2"	
repeat_region	/rpt family="MERS"	47500. .47781	
repeat_region	21861. .22013	/rpt family="Alu"	
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repeat_region	/rpt family="THE1"	49935. .50077	
repeat_region	23779. .23994	/rpt family="THE1"	
repeat_region	/note="GRAIL 2 excellent exon, frame 0"	50080. .51967	
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repeat_region	/rpt family="MLT1"	complement(50244. .50543)	
repeat_region	24957. .25094	/rpt family="Alu"	
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repeat_region	27635. .27825	/rpt family="THE1"	
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Query Match 92.4%; Score 19.4; DB 8; Length 60904;			
Best Local Similarity 95.2%; Pred. No. 86;			
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 GCAAGTGTCTAGTGTGGGG 21		
Db	14035 GCAAGTGTCTAGTGTGGGG 14055		
RESULT 39			
AP001609	AP001609	108927 bp	DNA linear PRI 03-JUN-2000
LOCUS	Homo sapiens genomic DNA, chromosome 21, clone:KB447A5, MX1-D21S171		
DEFINITION	region, complete sequence.		
ACCESSION	AP001609.1	GI:7670563	
VERSION	AP001609.1	GI:7670563	
KEYWORDS	HIG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primate; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 108927)		
AUTHORS	Shimizu.N., Kudoh.J. and Shibuya.K.		
TITLE	Homo sapiens genomic DNA, chromosome 21, clone:KB447A5, MX1-D21S171		
JOURNAL	Published Only in DataBase (2000)		
REFERENCE	2 (bases 1 to 108927)		
AUTHORS	Shimizu.N., Kudoh.J. and Shibuya.K.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-APR-2000) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)		

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FEATURES
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ORIGIN
  Query Match      92.4%; Score 19.4; DB 8; Length 108927;
  Best Local Similarity 95.2%; Pred. No. 86;
  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAAGTGTGTAGGTGCGGGG 21
        |||||
Db      28636  GCAAGTGTGTAGGTGCGGGG 28656

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DEFINITION Mus musculus clone CT7-9K21, WORKING DRAFT SEQUENCE, 62 unordered
            pieces.
ACCESSION  AC023611
VERSION    AC023611.2 GI:8810277
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Mus musculus (house mouse)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
  AUTHORS  DOE Joint Genome Institute.
  TITLE    Sequencing of Mouse
  JOURNAL  Unpublished
  REFERENCE 2 (bases 1 to 221285)
  AUTHORS  DOE Joint Genome Institute.
  TITLE    Direct Submission
  JOURNAL  Submitted (16-FEB-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            On Jun 29, 2000 this sequence version replaced gi:6980221.
  COMMENT  -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
            Project Information
            Center Project Name: 956898
            Center clone name: RG-MBAC_9K21
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            Summary Statistics
            Consensus quality: 172196 bases at least Q40
            Consensus quality: 196011 bases at least Q30
            Consensus quality: 201702 bases at least Q20
            Estimated insert size: 160000; pulse field gel estimation
            Estimated insert size: 215185; sum-of-contigs estimation
            Quality coverage: 6.26 in Q20 bases; pulse field gel estimation
            Quality coverage: 4.65 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 62 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            * 1 1033: contig of 1033 bp in length
            * 1034 1133: gap of unknown length
            * 1134 2542: contig of 1409 bp in length
            * 2543 2642: gap of unknown length
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            3698: contig of 1056 bp in length
            3798: gap of unknown length
            4993: contig of 1195 bp in length
            5093: gap of unknown length
            6427: contig of 1334 bp in length
            6527: gap of unknown length
            7763: contig of 1236 bp in length
            7863: gap of unknown length
            8877: contig of 1014 bp in length
            8878 8878: gap of unknown length
            10256: contig of 1279 bp in length
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            11357 11357: contig of 1000 bp in length
            11456: gap of unknown length
            12470: contig of 1014 bp in length
            12471 12471: gap of unknown length
            13611: contig of 1291 bp in length
            13621: gap of unknown length
            15060: contig of 1099 bp in length
            15160: gap of unknown length
            16252: contig of 1092 bp in length
            16352: gap of unknown length
            17470: contig of 1118 bp in length
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            18937: contig of 1267 bp in length
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            20246: contig of 1309 bp in length
            20346: gap of unknown length
            21515: contig of 1169 bp in length
            21516 21516: gap of unknown length
            22752: contig of 1137 bp in length
            22852: gap of unknown length
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            24539 24539: gap of unknown length
            25615: contig of 1077 bp in length
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            26918: contig of 1203 bp in length
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            35583 35583: gap of unknown length
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            46013: gap of unknown length
            47295: contig of 1282 bp in length
            47395: gap of unknown length
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            48601 48601: gap of unknown length
            50670: contig of 2070 bp in length
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* 56312 56411: gap of unknown length
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* 59167 59266: gap of unknown length
* 59267 62681: contig of 3415 bp in length
* 62682 62781: gap of unknown length
* 62782 65691: contig of 2910 bp in length
* 65692 65791: gap of unknown length
* 65792 69358: contig of 3567 bp in length
* 69359 69458: gap of unknown length
* 69459 71957: contig of 2499 bp in length
* 71958 72057: gap of unknown length
* 72058 76352: contig of 4295 bp in length
* 76353 76453: gap of unknown length
* 76453 79737: contig of 3285 bp in length
* 79738 79837: gap of unknown length
* 79838 86357: contig of 6520 bp in length
* 86358 86457: gap of unknown length
* 86458 90914: contig of 4457 bp in length
* 90915 91014: gap of unknown length
* 91015 96832: contig of 5818 bp in length
* 96833 103782: gap of unknown length
* 103783 103882: contig of 6850 bp in length
* 103883 110628: contig of 6746 bp in length
* 110629 110728: gap of unknown length
* 110729 116501: contig of 5773 bp in length
* 116502 123034: contig of 6433 bp in length
* 123035 123134: gap of unknown length
* 123135 130209: contig of 7075 bp in length
* 130210 130309: gap of unknown length
* 130310 141462: contig of 11153 bp in length
* 141463 141562: gap of unknown length
* 141563 149389: contig of 7827 bp in length
* 149390 149489: gap of unknown length
* 149490 157306: contig of 7817 bp in length
* 157307 157406: gap of unknown length
* 157407 167404: contig of 9998 bp in length
* 167405 167504: gap of unknown length
* 167505 185812: contig of 18308 bp in length
* 185813 185912: gap of unknown length
* 185913 205026: contig of 19114 bp in length
* 205027 205126: gap of unknown length
* 205127 221285: contig of 16159 bp in length.

FEATURES
source
1. .221285
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="Ct7-9K21"
/clone_lib="citbCJ7 mouse BAC library"
1034. .1133
/estimated_length=unknown
2543. .2642
/estimated_length=unknown
3699. 3798
/estimated_length=unknown
4994. .5093
/estimated_length=unknown
6428. .6527
/estimated_length=unknown
7764. 7863
/estimated_length=unknown
8878. .8977
/estimated_length=unknown
10257. .10356
/estimated_length=unknown
11357. .11456
/estimated_length=unknown
12471. .12570
/estimated_length=unknown

gap 13862. .13961
/estimated_length=unknown
gap 15061. .15160
/estimated_length=unknown

Query Match 92.4%; Score 19.4; DB 14; Length 221285;
Best Local Similarity 95.2%; Pred. No. 87;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTGTAGGTGCGGG 21
|||||
Db 11528 GCAAGTGTGAAGGTGCGGG 11508
|||||

RESULT 41
HS21C085 340000 bp DNA linear PRI 16-APR-2005
LOCUS Homo sapiens chromosome 21 segment HS21C085.
DEFINITION AL163285 AP001740 BA000005
ACCESSION AL163285.2 GI:7171394
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 340000)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstiek,G.,
Horisch,K., Brandt,P., Schaefer,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.L.
Direct Submission
Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
The Chromosome 21 Mapping and Sequencing Consortium consists of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagami-hara 228-8555, Japan,
* e.mail: sakaki@gs.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and
* Keio University School of Medicine, Dept. of Molecular Biology, *
Tokyo 160-8582, Japan,
* e.mail: ehimizu@mb-med.keio.ac.jp
* URL: http://adenine.dmb.med.keio.ac.jp/
and
* GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
* info.genome@gbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Ihnestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.de/.
Location/Qualifiers

FEATURES

source	1. .340000 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" 41. .47014 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="P141D16, 5' partial" /clone_lib="RPC11.3-5 PAC library" /note="Accession No. AJ011929" 41. .81445 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="P269A14, 5' partial" /clone_lib="RPC11.3-5 PAC library" /note="Accession No. AJ011929" 73773. .231461 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="P265B9" /clone_lib="RPC11.3-5 PAC library" /note="Accession No. AJ011929" 205693. .314721 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KB447A5" /clone_lib="Keio BAC library" /note="Accession No. AP001609" 228319. .268419 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="CIT2533B8, 3' partial" /clone_lib="CITB_HSP BAC library" /note="Accession No. AP001610" 259427. .282253 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="Q87D5" /clone_lib="L121NCO2-Q Cosmid library" /note="Accession No. AJ011929" 3304. .3525 /note="MER58A" /rpt_family="DNA/MER1_type" /rpt_type=DISPERSED	repeat_region	4254. .4579 /note="AluSx" /rpt_family="SINE/Alu" /rpt_type=DISPERSED 4693. .4768 /note="L1MC/D" /rpt_family="LINE/L1" /rpt_type=DISPERSED 5206. .5229 /note="(TTTTA)n" /rpt_family="Simple_repeat" /rpt_type=TANDEM complement(5230. .5510) /note="AluJb" /rpt_family="SINE/Alu" /rpt_type=DISPERSED 5518. .5541 /note="(T)n" /rpt_family="Simple_repeat" /rpt_type=TANDEM 5558. .5989 /note="Charlie7" /rpt_family="DNA/MER1_type" /rpt_type=DISPERSED complement(5996. .6135) /note="MIR" /rpt_family="SINE/MIR" /rpt_type=DISPERSED complement(6240. .6541) /note="AluSx" /rpt_family="SINE/Alu" /rpt_type=DISPERSED 7101. .7138 /note="(TTTA)n" /rpt_family="Simple_repeat" /rpt_type=TANDEM complement(7139. .7415) /note="L1PA5" /rpt_family="LINE/L1" /rpt_type=DISPERSED complement(8130. .8232) /note="L1PA5" /rpt_family="LINE/L1" /rpt_type=DISPERSED 8233. .8440 /note="L1PA5" /rpt_family="LINE/L1" /rpt_type=DISPERSED 8804. .9172 /note="MLT1B" /rpt_family="LTR/MaLR" /rpt_type=DISPERSED 11017. .11150 /note="MER5A" /rpt_family="DNA/MER1_type" /rpt_type=DISPERSED complement(11278. .11746) /note="L2" /rpt_family="LINE/L2" /rpt_type=DISPERSED complement(11736. .12306) /note="L2" /rpt_family="LINE/L2" /rpt_type=DISPERSED complement(12307. .12591) /note="AluSq" /rpt_family="SINE/Alu" /rpt_type=DISPERSED complement(12592. .12783) /note="L2"
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Query Match 92.4%; Score 19.4; DB 8; Length 340000;
Best Local Similarity 95.2%; Pred. No. 87;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGGG 21
|||||
Db 234375 GCAAGTGCTGCAGGTGCGGG 234395

RESULT 42
CR450734/c
LOCUS
DEFINITION
Zebrafish DNA sequence from clone DKEY-53N24 in linkage group 5,
complete sequence.

ACCESSION
CR450734
VERSION
HTG.
KEYWORDS
SOURCE
ORGANISM

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 69893)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (22-DEC-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 23, 2004 this sequence version replaced gi:56744163.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep/Clone-derived
Zebrafish pUC subclones occasionally display inconsistency over the
length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhiqiong Bao and Sean Eddy, submitted), and those
beginning 'drr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml DKEY-53N24
is from a Zebrafish BAC library
VECTOR: pIndigoBAC-5.

FEATURES
source
1..69893
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-53N24"
/clone_lib="DanioKey"

Query Match 87.6%; Score 18.4; DB 5; Length 69893;

Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGGG 20
|||||
Db 52563 GCAAGTGCTGTAGTGCTGG 52544

RESULT 43
AY448313/c
LOCUS
DEFINITION
Colobus guereza clone OLG_57 olfactory receptor-like protein gene,
partial sequence.

ACCESSION
AY448313
VERSION
AY448313.1 GI:38634341
KEYWORDS
SOURCE
ORGANISM

Colobus guereza (guereza)
Colobus guereza
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Colobinae; Colobus.
1 (bases 1 to 667)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
Loss of Olfactory Receptor Genes Coincides with the Acquisition of
Full Trichromatic Vision in Primates
PLoS Biol. 2 (1), 0120-0125 (2004)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
2 (bases 1 to 667)
Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
Direct Submission
Submitted (20-OCT-2003) Max Plank Institute for Evolutionary
Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
Location/Qualifiers

FEATURES
1..667
source

/organism="Colobus guereza"
/mol_type="genomic DNA"
/db_xref="taxon:33548"
/clone="OLG_57"
/note="sample obtained from Primate Genetics German
Primate Center in Goettingen, Germany"
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/gene="olfactory receptor-like protein"

gene

ORIGIN

Query Match 84.8%; Score 17.8; DB 8; Length 667;
Best Local Similarity 90.5%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGGG 21
|||||
Db 217 GCAGTGCTGTAGTGAGGGG 197

RESULT 44
AY448570/c
LOCUS
DEFINITION
Trachypithecus auratus clone OLG_18 olfactory receptor-like protein
gene, partial sequence.

ACCESSION
AY448570
VERSION
AY448570.1 GI:38634598
KEYWORDS
SOURCE
ORGANISM

Trachypithecus auratus (Javan langur)
Trachypithecus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Colobinae; Trachypithecus.
1 (bases 1 to 667)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
Loss of Olfactory Receptor Genes Coincides with the Acquisition of
Full Trichromatic Vision in Primates
PLoS Biol. 2 (1), 0120-0125 (2004)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
2 (bases 1 to 667)
Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
Direct Submission

JOURNAL Submitted (20-OCT-2003) Max Plank Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
FEATURES Location/Qualifiers
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 /organism="Trachypithecus auratus"
 /mol_type="genomic DNA"
 /db_xref="taxon:222416"
 /clone="OLG_18"
 /notes="sample obtained from Primate Genetics German Primate Center in Goettingen, Germany"
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 /gene="Olfactory receptor-like protein"
ORIGIN
 Query Match 84.8%; Score 17.8; DB 8; Length 667;
 Best Local Similarity 90.5%; Pred. No. 5.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 GCAAGTCTGTAGTGGGGG 21
 ||| ||||| ||||| |||||
 Db 217 GCAGGTGCTGTAGTGAGGG 197

RESULT 45
AF076122/c
LOCUS
DEFINITION AF076122 1047 bp DNA linear VRT 20-JUL-1999
 Scomberomorus maculatus isolate HB265-nd2 NADH dehydrogenase
 subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
 product.
ACCESSION AF076122
VERSION AF076122.1 GI:5531765
KEYWORDS
SOURCE mitochondrial Scomberomorus maculatus
ORGANISM Scomberomorus maculatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Perciformes; Perciformes;
 Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
 (Teleostei:Scombridae) species group: molecules, morphology and
 biogeography of Spanish mackerels
 Unpublished
JOURNAL 2 (bases 1 to 1047)
REFERENCE Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
AUTHORS Direct Submission
TITLE Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
 Institute, Unit 0948, APO, AA 34002-0948, USA
JOURNAL Location/Qualifiers
 1..1047
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 /organelle="mitochondrion"
 /mol_type="genomic DNA"
 /isolate="HB265-nd2"
 /db_xref="taxon:99344"
 1..1047
 /gene="ND2"
 1..1047
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 /translation=1
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 /protein_id="AAD4456.1"
 /db_xref="GI:5531781"
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 AQSHPRVAVATTKYFLTOATAAMLLFASTNAWLGTOWNIQQWTHPIPTTMIIL
 AKXIGHAPLWSLPEVLQGLDITGLISTWQKLAPFALIQHNSAPTMLMGVTS
 TLVGWGGLNQOLRIKLAYSSIAHLGWMILLIQFSPSLTLLTSTYILMTSATFLVF
 KLNKATNNMLATSWTKTIPALTALAPLISLGLGGLPPLTGTGFMKPKLILQELSQDILAP
 VATIAALSLSLYFTYLRLSYAMTLLTMSPNNLSTGTPWRLASNQLSLPISLFTVATIA
 LLPLTPALTATLTLT"
ORIGIN

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DEFINITION Scomberomorus regalis isolate STR13836-nd2 NADH dehydrogenase
            subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
            product.
ACCESSION AF076124.1 GI:5531767
VERSION AF076124
KEYWORDS mitochondrial Scomberomorus regalis
SOURCE Scomberomorus regalis
ORGANISM Scomberomorus regalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
            (Teleostei:Scombridae) species group: molecules, morphology and
            biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
            Research Institute, Unit 0948, APO, AA 34002-0948, USA
FEATURES
            source
            1..1047
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            /organelle="mitochondrion"
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            /isolate="STR13836-nd2"
            /db_xref="taxon:99345"
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            1..1047
            /gene="ND2"
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            /transl_table=2
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            /protein_id="AAD4458.1"
            /db_xref="GI:5531783"
            /translation="MNPYILATLLFGLIGLTTITTFASSHLLAWMGLEMTLIAIPLM
            AQSHHPRAVEATTKYFLQTATAAMLLFASTTNAWLTGWNIEQMHPTPTMIIAL
            ALKIGLAPHSWLPVQLGLDTTGLSTWOKLAPFALLIOMHSANPTMLIMLGVTG
            TLVGGGNGNQTLRKILAYSSIAHLGWMILIQSPSLTLLTYILMTSATPLVF
            KLNKATNINMLATSWTKPTALAPLVLLSGGUPPLTGFMFKMLIQELSKQDLAP
            VATLAALSALLSYFLRLSYAMTLTMSPNLSGTTTPWRLASNQLSLPLSLFIVATLA
            LPLTPALTITLTL"
            ORIGIN
            Query Match 84.8%; Score 17.8; DB 5; Length 1047;
            Best Local Similarity 90.5%; Pred. No. 5.6e+02;
            Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21
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Db 728 GCAAGGGCTGTAAGTGGGG 708

RESULT 48
AF076125/c 1047 bp DNA linear VRT 20-JUL-1999
LOCUS Scomberomorus maculatus isolate STR15090-nd2 NADH dehydrogenase
DEFINITION subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
            product.
ACCESSION AF076125.1 GI:5531768
VERSION AF076125
KEYWORDS mitochondrial Scomberomorus maculatus
SOURCE Scomberomorus maculatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
            (Teleostei:Scombridae) species group: molecules, morphology and
            biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
            Research Institute, Unit 0948, APO, AA 34002-0948, USA
FEATURES
            source
            1..1047
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            /organelle="mitochondrion"
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            /db_xref="taxon:99345"
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            1..1047
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            /protein_id="AAD4458.1"
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            AQSHHPRAVEATTKYFLQTATAAMLLFASTTNAWLTGWNIEQMHPTPTMIIAL
            ALKIGLAPHSWLPVQLGLDTTGLSTWOKLAPFALLIOMHSANPTMLIMLGVTG
            TLVGGGNGNQTLRKILAYSSIAHLGWMILIQSPSLTLLTYILMTSATPLVF
            KLNKATNINMLATSWTKPTALAPLVLLSGGUPPLTGFMFKMLIQELSKQDLAP
            VATLAALSALLSYFLRLSYAMTLTMSPNLSGTTTPWRLASNQLSLPLSLFIVATLA
            LPLTPALTITLTL"
            ORIGIN
            Query Match 84.8%; Score 17.8; DB 5; Length 1047;
            Best Local Similarity 90.5%; Pred. No. 5.6e+02;
            Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21
    ||||| ||||| ||||| ||||| |||||
Db 728 GCAAGGGCTGTAAGTGGGG 708

RESULT 48
AF076125/c 1047 bp DNA linear VRT 20-JUL-1999
LOCUS Scomberomorus maculatus isolate STR15090-nd2 NADH dehydrogenase
DEFINITION subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
            product.
ACCESSION AF076125.1 GI:5531768
VERSION AF076125
KEYWORDS mitochondrial Scomberomorus maculatus
SOURCE Scomberomorus maculatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
            (Teleostei:Scombridae) species group: molecules, morphology and
            biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
            Research Institute, Unit 0948, APO, AA 34002-0948, USA
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LOCUS Scomberomorus regalis isolate HB872-nd2 NADH dehydrogenase subunit
DEFINITION 2 gene, complete cds; mitochondrial gene for mitochondrial product.
ACCESSION AF076126
VERSION AF076126.1 GI:5531769
KEYWORDS mitochondrial Scomberomorus regalis
SOURCE Scomberomorus regalis
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            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
            (Teleostei:Scombridae) species group: molecules, morphology and
            biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
            Research Institute, Unit 0948, APO, AA 34002-0948, USA
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            Best Local Similarity 90.5%; Pred. No. 5.6e+02;
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Db 728 GCAAGGGCTGTAAGTGGGG 708

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ORIGIN

Query Match 84.8%; Score 17.8; DB 5; Length 1047;
Best Local Similarity 90.5%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
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Db 728 GCAAGGGCTGTAAGTGGGG 708

RESULT 50

AF076127/c

LOCUS

DEFINITION

1047 bp DNA linear VRT 20-JUL-1999
Scomberomorus maculatus isolate HB261-nd2 NADH dehydrogenase
subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
product.

ACCESSION

AF076127

VERSION

AF076127.1

KEYWORDS

SOURCE

ORGANISM

mitochondrion Scomberomorus maculatus

Scomberomorus maculatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Perciformes; Perciformes;

Scombroidei; Scombridae; Scomberomorus.

1 (bases 1 to 1047)

Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.

Phylogenetic systematics of the Scomberomorus regalis

(Teleostei:Scombridae) species group: molecules, morphology and

biogeography of Spanish mackerels

Unpublished

2 (bases 1 to 1047)

Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.

Direct Submission

Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical

Research Institute, Unit 0948, APO, AA 34002-0948, USA

Location/Qualifiers

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ORIGIN

Query Match 84.8%; Score 17.8; DB 5; Length 1047;
Best Local Similarity 90.5%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
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Db 728 GCAAGGGCTGTAAGTGGGG 708

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:45:58 ; Search time 72.5 Seconds
(without alignments)
514.880 Million cell updates/sec

Title: US-10-070-415A-37_COPY_410_430

Perfect score: 21

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19.4	92.4	581	3	US-09-813-031-2
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5	19.4	92.4	581	3	US-09-813-990A-1
6	19.4	92.4	581	3	US-09-813-990A-2
7	19.4	92.4	581	3	US-09-813-990A-3
8	19.4	92.4	581	3	US-09-813-990A-4
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10	17	81.0	3304	3	US-09-949-016-1888
11	17	81.0	49389	3	US-09-949-016-12547
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13	16.8	80.0	1972	3	US-09-857-5248-9
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15	16.8	80.0	5519	3	US-09-453-7028-226
16	16.8	80.0	5519	3	US-10-114-170-226
17	16.8	80.0	9072	3	US-08-956-171E-45
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21	16.2	77.1	601	3	US-09-949-016-188722
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23	16.2	77.1	601	3	US-09-949-016-192855
24	16.2	77.1	601	3	US-09-949-016-192901

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99 15.2 72.4 585 3 US-08-775-414-12 Sequence 12, Appl
100 15.2 72.4 585 3 US-08-931-858E-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-813-031-1
; Sequence 1, Application US/09813031
; Patent No. 6667155
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
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US-09-813-031-1

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Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 2
US-09-813-031-2
; Sequence 2, Application US/09813031
; Patent No. 6667155
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
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; ORGANISM: Homo sapiens
US-09-813-031-2

Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
US-09-813-031-3
; Sequence 3, Application US/09813031
; Patent No. 6667155
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
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US-09-813-031-3

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Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
DB 410 GCAAGTCTGMAGTGGGG 430

RESULT 4
US-09-813-031-4
; Sequence 4, Application US/09813031
; Patent No. 6667155
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT FILING DATE: 2001-03-21
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; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
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US-09-813-031-4

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Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Patent No. 6783935
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
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DB 410 GCAAGTGTCTAGGTGCGGG 430

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; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
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; US-09-813-990A-4

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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 9
US-09-949-016-805/c
; Sequence 805, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; US-09-813-990A-3
; Sequence 3, Application US/09813990A
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FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
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LENGTH: 3302
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US-09-949-016-805

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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Db 541 GTGCTGTAGTGGGGG 525

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US-09-949-016-1888/c
Sequence 1888, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
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ORGANISM: Human
US-09-949-016-1888

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Sequence 12547, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12547
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ORGANISM: Human
US-09-949-016-12547

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
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RESULT 12
US-09-949-016-13630/c
Sequence 13630, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13630
LENGTH: 49389
TYPE: DNA
ORGANISM: Human
US-09-949-016-13630

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 21458 GTGCTGTAGTGGGGG 21442

RESULT 13
US-09-857-524B-9/c
Sequence 9, Application US/09857524B
Patent No. 6864077
GENERAL INFORMATION:
APPLICANT: Edgar B. Cahoon
APPLICANT: Rebecca E. Cahoon
APPLICANT: William D. Hitz
APPLICANT: Anthony J. Kinney
TITLE OF INVENTION: Membrane-Bound Desaturases
FILE REFERENCE: BB1264
CURRENT APPLICATION NUMBER: US/09/857,524B
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,784
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO 9

```
; LENGTH: 1972
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-857-524B-9

Query Match      80.0%; Score 16.8; DB 3; Length 1972;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
   |||||
Db 829 GCAAGTGTCTAGGTGCGGG 810

RESULT 14
US-09-711-164-296/c
; Sequence 296, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; FILE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4134)
US-09-711-164-296

Query Match      80.0%; Score 16.8; DB 3; Length 4134;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
   |||||
Db 243 GTAAGTGTCTAGGTGCGGG 224

RESULT 15
US-09-453-702B-226/c
; Sequence 226, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 226:
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; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5519
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-453-702B-226

Query Match      80.0%; Score 16.8; DB 3; Length 5519;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
   |||||
Db 347 GTAAGTGTCTAGGTGCGGG 328

RESULT 16
US-10-114-170-226/c
; Sequence 226, Application US/10114170
; Patent No. 6855814
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 226:
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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 5519
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-10-114-170-226

Query Match      80.0%; Score 16.8; DB 3; Length 5519;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGCTGTAGTGCGGG 20
Db      347 GTAACGTGCTGTAGTGCGGG 328

RESULT 17
US-08-956-171E-45
; Sequence 45, Application US/08956171E
; Patent No. 6591114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9072 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-956-171E-45

Query Match      80.0%; Score 16.8; DB 3; Length 9072;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGCTGTAGTGCGGG 20

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Db      2901 GCAAGTTATGTAGTGCGGG 2920

RESULT 18
US-08-781-986A-45
; Sequence 45, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9072 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; US-08-781-986A-45

Query Match      80.0%; Score 16.8; DB 3; Length 9072;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGCTGTAGTGCGGG 20
Db      2901 GCAAGTTATGTAGTGCGGG 2920

RESULT 19
US-09-949-016-188624
; Sequence 188624, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

```


; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188624
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-188624

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 20
US-09-949-016-188673
; Sequence 188673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188673
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-188673

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 21
US-09-949-016-188722
; Sequence 188722, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188722
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-188722

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 22
US-09-949-016-188771
; Sequence 188771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188771
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-188771

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 23
US-09-949-016-192855
; Sequence 192855, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192855
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-192855

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATGCGGG 60

RESULT 24
US-09-949-016-192901
; Sequence 192901, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192901
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-192901

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATGCGGG 60

RESULT 25
US-09-949-016-192947
; Sequence 192947, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192947
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-192947

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATGCGGG 60

RESULT 26
US-09-949-016-192993
; Sequence 192993, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192993
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-192993

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATGCGGG 60

RESULT 27
US-09-949-016-193039
; Sequence 193039, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193039
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193039

Query Match 77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
||||| ||||| ||||| |||||
Db 40 GCAAGGGCTGTGGATGCGGG 60

RESULT 28
US-09-949-016-193132
; Sequence 193132, Application US/09949016
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193132
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193132

Query Match          77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 29
US-09-949-016-193225
; Sequence 193225, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193225
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193225

Query Match          77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 30
US-09-949-016-193318
; Sequence 193318, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193318
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193318

Query Match          77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 31
US-09-016-434-1413/C
; Sequence 1413, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1413:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9516319
US-09-016-434-1413
```

Query Match 77.1%; Score 16.2; DB 3; Length 1282;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 DB 572 GCGGGTCTGTAGTGGGGG 552

RESULT 32
 US-09-949-016-17236
 ; Sequence 17236, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17236
 ; LENGTH: 48682
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-17236

Query Match 77.1%; Score 16.2; DB 3; Length 48682;
 Best Local Similarity 85.7%; Pred. No. 4.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 DB 5084 GCAAGGCTGTGGATCGGGG 5104

RESULT 33
 US-09-949-016-17237
 ; Sequence 17237, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17237
 ; LENGTH: 48682
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-17237

Query Match 77.1%; Score 16.2; DB 3; Length 48682;
 Best Local Similarity 85.7%; Pred. No. 4.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21

Db 5084 GCAAGGCTGTGGATCGGGG 5104

RESULT 34
 US-09-949-016-17238
 ; Sequence 17238, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17238
 ; LENGTH: 48682
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-17238

Query Match 77.1%; Score 16.2; DB 3; Length 48682;
 Best Local Similarity 85.7%; Pred. No. 4.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 DB 5084 GCAAGGCTGTGGATCGGGG 5104

RESULT 35
 US-09-949-016-17239
 ; Sequence 17239, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17239
 ; LENGTH: 48682
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-17239

Query Match 77.1%; Score 16.2; DB 3; Length 48682;
 Best Local Similarity 85.7%; Pred. No. 4.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 DB 5084 GCAAGGCTGTGGATCGGGG 5104

RESULT 36

```
US-09-949-016-17135
; Sequence 17135, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17135
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17135

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGGCGGG 21
Db      5084 GCAAGGGCTGTGGATCGGGG 5104

RESULT 37
US-09-949-016-17136
; Sequence 17136, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17136
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17136

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGGCGGG 21
Db      5084 GCAAGGGCTGTGGATCGGGG 5104

RESULT 38
US-09-949-016-17137
; Sequence 17137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17137
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17137

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGGCGGG 21
Db      5084 GCAAGGGCTGTGGATCGGGG 5104

RESULT 39
US-09-949-016-17138
; Sequence 17138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17138
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17138

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGGCGGG 21
Db      5084 GCAAGGGCTGTGGATCGGGG 5104

RESULT 40
US-09-949-016-17240
; Sequence 17240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17240
; LENGTH: 86213
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17240

Query Match          77.1%; Score 16.2; DB 3; Length 86213;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
    ||||| ||||| ||||| |||||
Db 5084 GCAAGGCTGTGGATCGGG 5104

RESULT 41
US-09-949-016-17241
; Sequence 17241, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17241
; LENGTH: 86213
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17241

Query Match          77.1%; Score 16.2; DB 3; Length 86213;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
    ||||| ||||| ||||| |||||
Db 5084 GCAAGGCTGTGGATCGGG 5104

RESULT 42
US-09-949-016-17242
; Sequence 17242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

```

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17242
; LENGTH: 86213
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17242

Query Match          77.1%; Score 16.2; DB 3; Length 86213;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
    ||||| ||||| ||||| |||||
Db 5084 GCAAGGCTGTGGATCGGG 5104

RESULT 43
US-09-949-016-17243
; Sequence 17243, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17243
; LENGTH: 86213
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17243

Query Match          77.1%; Score 16.2; DB 3; Length 86213;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
    ||||| ||||| ||||| |||||
Db 5084 GCAAGGCTGTGGATCGGG 5104

RESULT 44
US-09-292-097-9
; Sequence 9, Application US/09292097B
; Patent No. 6322977
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TAPASIN-LIKE PROTEIN
; FILE REFERENCE: PC-0002 US
; CURRENT APPLICATION NUMBER: US/09/292,097B
; CURRENT FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2842166T6
; FEATURE:

```



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;
; FILING DATE: No. 5753488ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION:
;
US-08-465-388-43

Query Match 75.2%; Score 15.8; DB 2; Length 545;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGCGG 20
Db 116 CAAGTGCTGAAGTGCGG 98

RESULT 48
US-09-949-016-94093
; Sequence 94093, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94093
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94093

Query Match 75.2%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGG 19
Db 154 GCAAGTGCTGTAGTGCTG 172

RESULT 49
US-09-949-016-183284/c
; Sequence 183284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94093
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183284

Query Match 75.2%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGG 19
Db 154 GCAAGTGCTGTAGTGCTG 172

RESULT 49
US-09-949-016-183284/c
; Sequence 183284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183284
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183284

Query Match 75.2%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGTGCTGTAGTGCGGG 21
Db 419 AAGTGCTGTAGTGGAAGG 401

RESULT 50
US-08-840-683-2
; Sequence 2, Application US/08840683
; Patent No. 5821051
; GENERAL INFORMATION:
; APPLICANT: Androphy, Elliot J.
; APPLICANT: Chen, Jason J.
; TITLE OF INVENTION: B6-BINDING PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,683
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,059
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-840-683-2
```


Query Match 75.2%; Score 15.8; DB 2; Length 688;
 Best Local Similarity 89.5%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAAGTGTGTAGTGGGG 20
 ||||| ||||| ||||| |||||
 Db 600 CAAGTGTGTAGTGGGG 618

Search completed: January 27, 2006, 07:08:54
 Job time : 73.5 secs

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:44:44 ; Search time 396 Seconds
(without alignments)
44.051 Million cell updates/sec

Title: US-10-070-415A-37_COPY_410_430

Perfect score: 21
Sequence: 1 gcaagtctgttagtgcgggg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_NA_New.*
1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.2	77.1	270	8	US-11-043-752-2597
2	16.2	77.1	1090	7	US-10-750-185-35695
3	16.2	77.1	1090	7	US-10-750-623-36139
4	16.2	77.1	42823	8	US-11-066-725-18
5	16.2	77.1	163162	8	US-11-121-086-66
6	15.4	73.3	21	7	US-10-310-914A-145269
7	15.4	72.4	25	8	US-11-136-527-306462
8	15.2	72.4	489	8	US-11-136-527-3610
9	15.2	72.4	489	8	US-11-136-527-7706
10	15.2	72.4	636	7	US-10-793-626-743
11	15.2	72.4	870	7	US-10-793-626-63
12	15.2	72.4	1400	8	US-11-136-527-6488
13	15.2	72.4	1635	6	US-10-978-927-4
14	15.2	72.4	1635	6	US-10-978-927-11
15	15.2	72.4	1671	7	US-10-821-234-657
16	15.2	72.4	1857	6	US-10-978-927-16
17	15.2	72.4	1857	7	US-10-947-249-196
18	15.2	72.4	2094	7	US-10-750-185-31951
19	15.2	72.4	2094	7	US-10-750-623-31951
20	15.2	72.4	3032	7	US-10-793-626-3824
21	15.2	72.4	3370	7	US-10-793-626-4190
22	15.2	72.4	3374	8	US-11-136-527-2392

C 23	15.2	72.4	4019	7	US-10-793-626-4210	Sequence 4210, Ap
C 24	15.2	72.4	4020	7	US-10-750-185-36139	Sequence 36139, A
C 25	15.2	72.4	4020	7	US-10-750-623-36139	Sequence 36139, A
C 26	15.2	72.4	4036	7	US-10-793-626-4287	Sequence 4287, Ap
C 27	15.2	72.4	11110	6	US-10-978-927-20	Sequence 20, Appl
C 28	15.2	72.4	12863	6	US-10-978-927-19	Sequence 19, Appl
C 29	15.2	72.4	23907	8	US-11-186-731-4	Sequence 4, Appl
C 30	15.2	72.4	24120	8	US-11-186-731-4	Sequence 4, Appl
C 31	15.2	72.4	175673	8	US-11-121-086-55	Sequence 55, Appl
C 32	15.2	72.4	285300	7	US-10-857-780-6	Sequence 6, Appl
C 33	15.2	72.4	1691140	8	US-11-091-018-1	Sequence 1, Appl
C 34	14.8	70.5	874	7	US-10-750-185-47833	Sequence 47833, A
C 35	14.8	70.5	874	7	US-10-750-623-47833	Sequence 47833, A
C 36	14.8	70.5	1187	7	US-10-750-185-46874	Sequence 46874, A
C 37	14.8	70.5	1187	7	US-10-750-623-46874	Sequence 46874, A
C 38	14.8	70.5	1258	7	US-10-750-185-46077	Sequence 46077, A
C 39	14.8	70.5	1258	7	US-10-750-623-46077	Sequence 46077, A
C 40	14.8	70.5	1321	7	US-10-750-185-63637	Sequence 63637, A
C 41	14.8	70.5	1321	7	US-10-750-623-63637	Sequence 63637, A
C 42	14.8	70.5	1444	8	US-11-000-688-138	Sequence 138, App
C 43	14.8	70.5	3331	7	US-10-750-185-41819	Sequence 41819, A
C 44	14.8	70.5	3331	7	US-10-750-623-41819	Sequence 41819, A
C 45	14.8	70.5	3404	7	US-10-750-185-52746	Sequence 52746, A
C 46	14.8	70.5	3404	7	US-10-750-623-52746	Sequence 52746, A
C 47	14.8	70.5	7142	7	US-10-516-768-22	Sequence 22, Appl
C 48	14.6	69.5	201	7	US-10-995-561-65200	Sequence 65200, A
C 49	14.6	69.5	201	7	US-10-995-561-82368	Sequence 82368, A
C 50	14.6	69.5	201	7	US-10-995-561-82380	Sequence 82380, A
C 51	14.6	69.5	600	8	US-11-136-527-7944	Sequence 7944, Ap
C 52	14.6	69.5	618	8	US-11-136-527-3948	Sequence 3948, Ap
C 53	14.6	69.5	975	7	US-10-750-185-41153	Sequence 41153, A
C 54	14.6	69.5	975	7	US-10-750-623-41153	Sequence 41153, A
C 55	14.6	69.5	1007	5	US-09-978-360A-377	Sequence 377, App
C 56	14.6	69.5	1103	7	US-10-750-185-41938	Sequence 41938, A
C 57	14.6	69.5	1103	7	US-10-750-623-41938	Sequence 41938, A
C 58	14.6	69.5	1160	7	US-10-750-185-26499	Sequence 26499, A
C 59	14.6	69.5	1160	7	US-10-750-623-26499	Sequence 26499, A
C 60	14.6	69.5	1243	7	US-10-750-185-63749	Sequence 63749, A
C 61	14.6	69.5	1243	7	US-10-750-623-63749	Sequence 63749, A
C 62	14.6	69.5	1277	7	US-10-750-185-53108	Sequence 53108, A
C 63	14.6	69.5	1277	7	US-10-750-623-53108	Sequence 53108, A
C 64	14.6	69.5	1291	7	US-10-750-185-62669	Sequence 62669, A
C 65	14.6	69.5	1291	7	US-10-750-623-62669	Sequence 62669, A
C 66	14.6	69.5	1329	7	US-10-750-185-34351	Sequence 34351, A
C 67	14.6	69.5	1329	7	US-10-750-623-34351	Sequence 34351, A
C 68	14.6	69.5	1335	7	US-10-750-185-27628	Sequence 27628, A
C 69	14.6	69.5	1335	7	US-10-750-623-27628	Sequence 27628, A
C 70	14.6	69.5	1382	7	US-10-750-185-42137	Sequence 42137, A
C 71	14.6	69.5	1382	7	US-10-750-623-42137	Sequence 42137, A
C 72	14.6	69.5	1558	7	US-10-750-185-42718	Sequence 42718, A
C 73	14.6	69.5	1558	7	US-10-750-623-42718	Sequence 42718, A
C 74	14.6	69.5	1605	7	US-10-750-185-53178	Sequence 53178, A
C 75	14.6	69.5	1605	7	US-10-750-623-53178	Sequence 53178, A
C 76	14.6	69.5	1795	7	US-10-750-185-56552	Sequence 56552, A
C 77	14.6	69.5	1795	7	US-10-750-623-56552	Sequence 56552, A
C 78	14.6	69.5	1974	7	US-10-750-185-27606	Sequence 27606, A
C 79	14.6	69.5	1974	7	US-10-750-623-27606	Sequence 27606, A
C 80	14.6	69.5	1976	7	US-10-750-185-63562	Sequence 63562, A
C 81	14.6	69.5	1976	7	US-10-750-623-63562	Sequence 63562, A
C 82	14.6	69.5	2122	7	US-10-821-234-131	Sequence 131, App
C 83	14.6	69.5	2438	7	US-10-750-185-53163	Sequence 53163, A
C 84	14.6	69.5	2438	7	US-10-750-623-53163	Sequence 53163, A
C 85	14.6	69.5	2793	7	US-10-775-169-328	Sequence 228, App
C 86	14.6	69.5	2849	7	US-10-131-826A-171	Sequence 371, App
C 87	14.6	69.5	3177	8	US-11-108-528-41	Sequence 41, Appl
C 88	14.6	69.5	4402	8	US-11-136-527-2389	Sequence 2389, Ap
C 89	14.6	69.5	26737	7	US-10-995-561-13496	Sequence 13496, A
C 90	14.6	69.5	35344	7	US-10-995-561-13307	Sequence 13307, A
C 91	14.6	69.5	66916	7	US-10-995-561-13374	Sequence 13374, A
C 92	14.6	69.5	98345	8	US-11-112-908-35	Sequence 36, Appl
C 93	14.6	69.5	100000	8	US-11-124-368A-2881	Sequence 2881, Ap
C 94	14.6	69.5	127340	8	US-11-113-908-35	Sequence 35, Appl
C 95	14.6	69.5	153376	8	US-11-121-086-5	Sequence 5, Appl

c 96 14.6 69.5 168516 8 US-11-121-086-3 Sequence 3, Appli
c 97 14.6 69.5 1080000 7 US-10-928-446A-1 Sequence 1, Appli
c 98 14.6 69.5 1080000 7 US-10-928-446A-181 Sequence 181, App
c 99 14.6 69.5 1080000 7 US-10-928-446A-183 Sequence 183, App
c 100 14.6 69.5 1080000 7 US-10-928-446A-185 Sequence 185, App

ALIGNMENTS

RESULT 1
US-11-043-752-2597
; Sequence 2597, Application US/11043752
; Publication No. US20060014165A1
; GENERAL INFORMATION:
; APPLICANT: Hakonarson, Hakon
; APPLICANT: Gurney, Mark E.
; APPLICANT: Halepl, Eva
; TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT FOR
; TITLE OF INVENTION: ASTHMA AND OTHER RESPIRATORY DISEASES BASED ON HAPLOTYPE
; FILE REFERENCE: 2345.2044-003
; CURRENT APPLICATION NUMBER: US/11/043,752
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/US04/022446
; PRIOR FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: 60/487,072
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/559,611
; PRIOR FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 4326
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2597
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-043-752-2597

Query Match 77.1%; Score 16.2; DB 8; Length 270;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTCTAGTGGCGGG 21
|||||
Db 242 GCAAGTCTCTGGAGCTGGG 262

RESULT 2
US-10-750-185-35695/c
; Sequence 35695, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35695
; LENGTH: 1090
; TYPE: DNA
; ORGANISM: Bovine 19866881301896
US-10-750-185-35695

Query Match 77.1%; Score 16.2; DB 7; Length 1090;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTCTAGTGGCGGG 21
|||||
Db 857 GCAGGTGCTGCGGTGCGGG 837

RESULT 3
US-10-750-623-35695/c
; Sequence 35695, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35695
; LENGTH: 1090
; TYPE: DNA
; ORGANISM: Bovine 19866881301896
US-10-750-623-35695

Query Match 77.1%; Score 16.2; DB 7; Length 1090;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTCTAGTGGCGGG 21
|||||
Db 857 GCAGGTGCTGCGGTGCGGG 837

RESULT 4
US-11-066-725-18/c
; Sequence 18, Application US/11066725
; Publication No. US20050272680A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Xing-Xian Yu
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US.C1
; CURRENT APPLICATION NUMBER: US/11/066,725
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: US/10/643,801
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: PCT/US2004/024384
; PRIOR FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 492
; SEQ ID NO 18
; LENGTH: 42823
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-11-066-725-18

Query Match 77.1%; Score 16.2; DB 8; Length 42823;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

US-11-136-527-7706

Query Match 72.4%; Score 15.2; DB 8; Length 489;
Best Local Similarity 85.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGG 20
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Db 356 GCAAGAGCTGTGGCGGG 375

RESULT 10

US-10-793-626-743
; Sequence 743, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 743
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-743

Query Match 72.4%; Score 15.2; DB 7; Length 636;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGG 20
||||| ||||| ||||| |||||

Db 457 GCAAGTTATGTAGTGCGG 476

RESULT 11

US-10-793-626-63
; Sequence 63, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-63

Query Match 72.4%; Score 15.2; DB 7; Length 870;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGG 20
||||| ||||| ||||| |||||

Db 691 GCAAGTTATGTAGTGCGG 710

RESULT 12

US-11-136-527-6488
; Sequence 6488, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6488
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6488

Query Match 72.4%; Score 15.2; DB 8; Length 1400;
Best Local Similarity 85.0%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGG 20
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Db 438 GCAAGGGCTGTAGTTCTGG 457

RESULT 13

US-10-978-927-4
; Sequence 4, Application US/10978927
; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-4

Query Match 72.4%; Score 15.2; DB 6; Length 1635;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGG 20
||||| ||||| ||||| |||||

Db 1480 GCAAGTGCTGTGTGTGAGAG 1499

RESULT 14

US-10-978-927-11
; Sequence 11, Application US/10978927
; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos

;; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
;; FILE OF INVENTION: BETA-HEXOSAMINIDASE
;; FILE REFERENCE: 21108.0018U2
;; CURRENT APPLICATION NUMBER: US/10/978,927
;; CURRENT FILING DATE: 2004-11-01
;; PRIOR APPLICATION NUMBER: PCT/US03/13672
;; PRIOR FILING DATE: 2003-05-02
;; PRIOR APPLICATION NUMBER: 60/377,503
;; PRIOR FILING DATE: 2002-05-02
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 1635
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:/Note =
;; OTHER INFORMATION: Synthetic Construct
US-10-978-927-11

Query Match 72.4%; Score 15.2; DB 6; Length 1635;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 20
|||||
Db 1480 GCAAGTGTCTGTGGTGAGAG 1499

RESULT 15
US-10-821-234-657
;; Sequence 657, Application US/10821234
;; Publication No. US20050255114A1
;; GENERAL INFORMATION:
;; APPLICANT: Labat, Ivan
;; APPLICANT: Stache-Crain, Birgit
;; APPLICANT: Andarmani, Susan
;; APPLICANT: Tang, Y. Tom
;; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclapsia
;; FILE REFERENCE: 821A
;; CURRENT APPLICATION NUMBER: US/10/821,234
;; CURRENT FILING DATE: 2004-04-07
;; PRIOR APPLICATION NUMBER: US 60/462,047
;; PRIOR FILING DATE: 2003-04-07
;; NUMBER OF SEQ ID NOS: 1704
;; SOFTWARE: pt SEQ_genes Version 1.0
;; SEQ ID NO 657
;; LENGTH: 1671
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-821-234-657

Query Match 72.4%; Score 15.2; DB 7; Length 1671;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 20
|||||
Db 1516 GCAAGTGTCTGTGGTGAGAG 1535

RESULT 16
US-10-978-927-16
;; Sequence 16, Application US/10978927
;; Publication No. US2006009406A1
;; GENERAL INFORMATION:
;; APPLICANT: Kyrkanides, Stephanos
;; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
;; FILE OF INVENTION: BETA-HEXOSAMINIDASE
;; FILE REFERENCE: 21108.0018U2
;; CURRENT APPLICATION NUMBER: US/10/978,927
;; CURRENT FILING DATE: 2004-11-01
;; PRIOR APPLICATION NUMBER: PCT/US03/13672

;; PRIOR FILING DATE: 2003-05-02
;; PRIOR APPLICATION NUMBER: 60/377,503
;; PRIOR FILING DATE: 2002-05-02
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16
;; LENGTH: 1857
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:/Note =
;; OTHER INFORMATION: Synthetic Construct
US-10-978-927-16

Query Match 72.4%; Score 15.2; DB 6; Length 1857;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 20
|||||
Db 1591 GCAAGTGTCTGTGGTGAGAG 1610

RESULT 17
US-10-947-249-196
;; Sequence 196, Application US/10947249
;; Publication No. US20050287541A1
;; GENERAL INFORMATION:
;; APPLICANT: Akira NAKAGAWARA
;; APPLICANT: Miki OHIRA
;; APPLICANT: Shin ISHII
;; APPLICANT: Takeshi GOTO
;; APPLICANT: Hiroyuki KUBO
;; APPLICANT: Takahiro HIRATA
;; APPLICANT: Yasuko YOSHIDA
;; APPLICANT: Saichi YAMADA
;; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Me
;; FILE OF INVENTION: Predicting the Prognosis of Neuroblastoma
;; FILE REFERENCE: 117007
;; CURRENT APPLICATION NUMBER: US/10/947,249
;; CURRENT FILING DATE: 2004-09-23
;; PRIOR APPLICATION NUMBER: US 60/505,614
;; PRIOR APPLICATION NUMBER: 2003-09-25
;; NUMBER OF SEQ ID NOS: 200
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 196
;; LENGTH: 1857
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-947-249-196

Query Match 72.4%; Score 15.2; DB 7; Length 1857;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 20
|||||
Db 1591 GCAAGTGTCTGTGGTGAGAG 1610

RESULT 18
US-10-750-185-31951/c
;; Sequence 31951, Application US/10750185
;; Publication No. US20050260603A1
;; GENERAL INFORMATION:
;; APPLICANT: MMI GENOMICS, INC.
;; APPLICANT: Denise, Sue K.
;; APPLICANT: KERR, Richard
;; APPLICANT: ROSENFELD, David
;; APPLICANT: HOLM, Tom
;; APPLICANT: BATES, Stephen
;; APPLICANT: FANTIN, Dennis
;; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

```

; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31951
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-31951

```

Query Match	72.4%;	Score 15.2;	DB 7;	Length 2094;
Best Local Similarity	85.0%;	Pred. NO. 4.9e+02;		
Matches 17: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 GCAAGTGTCTAGGTGCGG 20
1613 GCAAGTGTCTCCAGGTGCAGG 1594

```

RESULT 19
US-10-750-623-31951/c
; Sequence 31951, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 31951
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-31951

```

Query Match	72.4%	Score 15.2;	DB 7;	Length 2094;
Best Local Similarity	85.0%	Pred. No. 4.9e+02;		
Matches 17: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 GCAAGTCTGTAGTGGG 20
|||
1613 GCAAGTCTCCAGGTGCGG 1594
Db

```

RESULT 20
US-10-793-626-3924/c
; Sequence 3924, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3924
; LENGTH: 3032

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3924

```

```
Query Match          72.4%; Score 15.2; DB 7; Length 3032;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1 GCAAGTGTCTAGGTGCGGG 20
1352 GCAAGTTATGTAGGTGCAGG 1333
pb

```

RESULT 21
US-10-793-626-4190
US-10-793-626-4190
; Sequence 4190, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4190
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4190

```

Query Match	72.4%	Score 15.2;	DB 7;	Length 3370;
Best Local Similarity	85.0%	Pred. No. 5.1e+02;		
Matches 17: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGG 20
pβ 1288 GCAAGTTATGTAGGTGCAGG 1307

```

RESULT 22
US-11-136-527-2392
; Sequence 2392, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2392
; LENGTH: 3374
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2392

```

Query Match	72.4%	Score 15.2;	DB 8;	Length 3374;
Best Local Similarity	85.0%	Pred. No. 5.1e+02;		
Matches 17; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 GCAAGTGTCTAGGTGGG 20
|||||
Db 2412 GCAAGGCTGTAGGTCTGG 2431

RESULT 23

US-10-793-626-4210/c
; Sequence 4210, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4210
; LENGTH: 4019
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4210

Query Match 72.4%; Score 15.2; DB 7; Length 4019;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGGG 20
|||||
Db 943 GCAAGTTATGTAGGTGAGG 924

RESULT 24

US-10-750-185-36139/c
; Sequence 36139, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36139
; LENGTH: 4020
; TYPE: DNA
; ORGANISM: Bovine 19866881456963
US-10-750-185-36139

Query Match 72.4%; Score 15.2; DB 7; Length 4020;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAAAGTGTGTAGGTGGGG 21
|||||
Db 3278 CAAAGTGTGGAGGTGAGG 3259

RESULT 25

US-10-750-623-36139/c

; Sequence 36139, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36139
; LENGTH: 4020
; TYPE: DNA
; ORGANISM: Bovine 19866881456963
US-10-750-623-36139

Query Match 72.4%; Score 15.2; DB 7; Length 4020;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAAAGTGTGTAGGTGGGG 21
|||||
Db 3278 CAAAGTGTGGAGGTGAGG 3259

RESULT 26

US-10-793-626-4287/c
; Sequence 4287, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4287
; LENGTH: 4036
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4287

Query Match 72.4%; Score 15.2; DB 7; Length 4036;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTGTAGGTGGGG 20
|||||
Db 2681 GCAAGTTATGTAGGTGAGG 2662

RESULT 27

US-10-978-927-20
; Sequence 20, Application US/10978927
; Publication No. US2006009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF


```

; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 55
; LENGTH: 175673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-55

```

```
Query Match          72.4%; Score 15.2; DB 8; Length 175673;
Best Local Similarity 85.0%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 2 CAAGTGTCTAGGTGCGGG 21
 |||||
 Db 12882 CAAGTGTCTAGGTGCGGG 128863

RESULT 32

```

US-5011-32
; US-10-857-780-6/c
; Sequence 6, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: THEOFOF
; FILE REFERENCE: SEQ-4069-CF
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 285300

```

```
; NAME/KEY: misc_feature
; LOCATION: (250575)..(250575)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature

Query Match      72.4%; Score 15.2; DB 7; Length 285300;
Best Local Similarity 85.0%; Pred. No. 7e+02; Indels 0;
Matches 17; Conservative 0; Mismatches 3;

QY      2 CAAAGTCTGTAGTGCGGG 21
       ||||| ||||||| |||
Db      255080 CAAGCACTGTAGTGTCGG 255061

RESULT 33
US-11-091-018-1/c
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Thetarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; METHOD OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1

Query Match      72.4%; Score 15.2; DB 8; Length 169114
Best Local Similarity 85.0%; Pred. No. 4.2e+02; Indels 0;
Matches 17; Conservative 0; Mismatches 3;

QY      1 GCAAGTGTCTAGTGTCGGG 20
       ||||| ||||||| |||
Db      421452 GCAAGTGCAGGAGTGTCGG 421433

RESULT 34
US-10-750-185-47833
; Sequence 47833, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNise, Sue K.
; APPLICANT: Kerr, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
```

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47833
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Bovine 19866881262435
US-10-750-185-47833

Query Match 70.5%; Score 14.8; DB 7; Length 874;
Best Local Similarity 88.9%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGCGG 19
|||||
DB 221 CAAGAGCTGTAGGTGAGG 238

RESULT 35

US-10-750-623-47833
; Sequence 47833, Application US/10/750,623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47833
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Bovine 19866881262435
US-10-750-623-47833

Query Match 70.5%; Score 14.8; DB 7; Length 874;
Best Local Similarity 88.9%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGCGG 19
|||||
DB 221 CAAGAGCTGTAGGTGAGG 238

RESULT 36

US-10-750-185-46874/c
; Sequence 46874, Application US/10/750,185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46874
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Bovine 19866880774723
US-10-750-185-46874

Query Match 70.5%; Score 14.8; DB 7; Length 1187;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGCGG 19
|||||
DB 185 CAAATGCTATAGTGCGG 168

RESULT 37

US-10-750-623-46874/c
; Sequence 46874, Application US/10/750,623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46874
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Bovine 19866880774723
US-10-750-623-46874

Query Match 70.5%; Score 14.8; DB 7; Length 1187;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGCGG 19
|||||
DB 185 CAAATGCTATAGTGCGG 168

RESULT 38

US-10-750-185-46077
; Sequence 46077, Application US/10/750,185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

```
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46077
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Bovine 19866881551932
US-10-750-185-46077

Query Match          70.5%; Score 14.8; DB 7; Length 1258;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGCG 18
    |||||
Db 183 GCAAGTGCTGGAGGTGG 200

RESULT 39
US-10-750-623-46077
; Sequence 46077, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46077
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Bovine 19866881551932
US-10-750-623-46077

Query Match          70.5%; Score 14.8; DB 7; Length 1258;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGCG 18
    |||||
Db 183 GCAAGTGCTGGAGGTGG 200

RESULT 40
US-10-750-185-63637/c
; Sequence 63637, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 63637
```

```
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880725092
US-10-750-185-63637

Query Match          70.5%; Score 14.8; DB 7; Length 1321;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACTGCTGTAGGTGCGGG 21
    |||||
Db 838 AGTGGTATAGGTGCGGG 821

RESULT 41
US-10-750-623-63637/c
; Sequence 63637, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 63637
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880725092
US-10-750-623-63637

Query Match          70.5%; Score 14.8; DB 7; Length 1321;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGTGTAGGTGCGGG 21
    |||||
Db 838 AGTGGTATAGGTGCGGG 821

RESULT 42
US-11-000-688-138/c
; Sequence 138, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 138
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc_feature
```

; LOCATION: (1)..(1444)
; OTHER INFORMATION: spi-b transcription factor (spi-1/pu.1
; OTHER INFORMATION: related (SPiB) gene.
US-11-000-688-138

Query Match 70.5%; Score 14.8; DB 8; Length 1444;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGGCGGG 21
||| ||||| ||||| |||||
Db 260 AGGGCTGTAGTGGCGGG 243

RESULT 43

US-10-750-185-41819/c
; Sequence 41819, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 41819
; LENGTH: 3331
; TYPE: DNA
; ORGANISM: Bovine 19866880995190

US-10-750-185-41819

Query Match 70.5%; Score 14.8; DB 7; Length 3331;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGGCGGG 21
||| ||||| ||||| |||||
Db 2671 ACTGCTGTAGTGGCGGG 2654

RESULT 44

US-10-750-623-41819/c
; Sequence 41819, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 41819
; LENGTH: 3331
; TYPE: DNA
; ORGANISM: Bovine 19866880995190

US-10-750-185-41819

US-10-750-623-41819

Query Match 70.5%; Score 14.8; DB 7; Length 3331;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGGCGGG 21
||| ||||| ||||| |||||
Db 2671 ACTGCTGTAGTGGCGGG 2654

RESULT 45

US-10-750-185-52746
; Sequence 52746, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 52746
; LENGTH: 3404
; TYPE: DNA
; ORGANISM: Bovine 19866881067975

US-10-750-185-52746

Query Match 70.5%; Score 14.8; DB 7; Length 3404;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGGCGGG 21
||| ||||| ||||| |||||
Db 1817 AGTGCTTTAGTGGTGGG 1834

RESULT 46

US-10-750-623-52746
; Sequence 52746, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 52746
; LENGTH: 3404
; TYPE: DNA
; ORGANISM: Bovine 19866881067975

US-10-750-623-52746

Query Match 70.5%; Score 14.8; DB 7; Length 3404;

Best Local Similarity 88.9%; Pred. No. 7.9e+02; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGTCTAGTGTGGGG 21

Db 1817 AGTGTCTAGTGTGGG 1834

RESULT 47

US-10-516-768-22

; Sequence 22, Application US/10516768

; Publication No. US20050256302A1

; GENERAL INFORMATION:

; APPLICANT: MINAMINO, NAOTO

; APPLICANT: KATAFUCHI, TAKESHI

; TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY

; FILE REFERENCE: 62273(71526)

; CURRENT APPLICATION NUMBER: US/10/516,768

; PRIOR FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: PCT/JP03/06641

; PRIOR FILING DATE: 2003-05-28

; PRIOR APPLICATION NUMBER: JP 2002-162797

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn ver. 3.3

; SEQ ID NO 22

; LENGTH: 7142

; TYPE: DNA

; ORGANISM: Sus sp.

US-10-516-768-22

Query Match

Best Local Similarity 70.5%; Score 14.8; DB 7; Length 7142;

Mismatches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAAGTCTAGTGTGGG 19

Db 5887 CATGTGCTGAGGTGGG 5904

RESULT 48

US-10-995-561-65200

; Sequence 65200, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; PRIOR FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 65200

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-65200

Query Match

Best Local Similarity 69.5%; Score 14.6; DB 7; Length 201;

Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTCTAGTGTGGGG 21

Db 104 GCAAGTCTAGTGTGGGG 124

RESULT 49

US-10-995-561-82368/c

; Sequence 82368, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 82368

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-82368

Query Match

Best Local Similarity 81.0%; Score 14.6; DB 7; Length 201;

Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTCTAGTGTGGGG 21

Db 65 GCAGGTCTGAGGTCCGGTG 45

RESULT 50

US-10-995-561-82380/c

; Sequence 82380, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 82380

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-82380

Query Match

Best Local Similarity 69.5%; Score 14.6; DB 7; Length 201;

Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTCTAGTGTGGGG 21

Db 33 GCAGGTCTGAGGTCCGGTG 13

Search completed: January 27, 2006, 07:33:57

Job time : 398 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:45:58 ; Search time 72.5 Seconds
(without alignments)
514.880 Million cell updates/sec

Title: us-10-070-415A-1

Perfect score: 21
Sequence: 1 cccgtgaggaactwctgtct 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA.*

1: /cgn2_6/prodata1/ina/1 COMB.seq.*
2: /cgn2_6/prodata1/ina/5 COMB.seq.*
3: /cgn2_6/prodata1/ina/6A COMB.seq.*
4: /cgn2_6/prodata1/ina/6B COMB.seq.*
5: /cgn2_6/prodata1/ina/H COMB.seq.*
6: /cgn2_6/prodata1/ina/PTUS COMB.seq.*
7: /cgn2_6/prodata1/ina/PR COMB.seq.*
8: /cgn2_6/prodata1/ina/RE COMB.seq.*
9: /cgn2_6/prodata1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20.6	98.1	25	3	US-09-782-361-1
2	20.6	98.1	27	2	US-08-256-568B-1
3	20.6	98.1	27	3	US-09-038-369B-1
4	20.6	98.1	27	3	US-09-378-900A-1
5	20.6	98.1	27	3	US-09-899-044-1
6	20.6	98.1	27	3	US-09-899-302-1
7	20.6	98.1	27	3	US-09-899-082B-1
8	20.6	98.1	28	3	US-08-474-700B-2
9	20.6	98.1	28	3	US-08-474-700B-29
10	20.6	98.1	28	6	PCT-US95-05812-2
11	20.6	98.1	28	6	PCT-US95-05812-29
12	20.6	98.1	45	2	US-08-690-495-22
13	20.6	98.1	45	3	US-08-690-494-22
14	20.6	98.1	45	3	US-09-299-217-22
15	20.6	98.1	45	3	US-09-728-265-22
16	20.6	98.1	45	3	US-10-309-438-22
17	20.6	98.1	45	6	PCT-US95-07671-22
18	20.6	98.1	45	8	US-09-798-641-22
19	20.6	98.1	51	2	US-08-356-287-31
20	20.6	98.1	51	6	PCT-US93-04863-31
21	20.6	98.1	67	3	US-08-474-700B-42
22	20.6	98.1	155	3	US-08-474-700B-41
23	20.6	98.1	242	2	US-08-335-595-1
24	20.6	98.1	260	3	US-08-474-700B-40

98 20.6 98.1 8638 3 US-10-309-561A-7 Sequence 7, Appli
99 20.6 98.1 8638 3 US-10-309-561A-24 Sequence 24, Appl
100 20.6 98.1 8638 3 US-10-309-561A-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-782-361-1
; Sequence 1, Application US/09782361
; Patent No. 6811974
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-47570S
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sense universal primer for PCR (first round)
US-09-782-361-1

Query Match 98.1%; Score 20.6; DB 3; Length 25;
Best Local Similarity 95.2%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTGTGAGGAAGTCTGTCT 21
Db 4 CCCTGTGAGGAAGTCTGTCT 24
|||||
|||||

RESULT 2
US-08-256-568B-1
; Sequence 1, Application US/08256568B
; Patent No. 5846704
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,568B
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992

Query Match 98.1%; Score 20.6; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
|||||

RESULT 3
US-09-038-369B-1
; Sequence 1, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,369B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: HCV
MAP POSITION: Position -299 of 5' end
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..27
OTHER INFORMATION: /standard name=
OTHER INFORMATION: "Universal HCV primer HcPr98"
US-08-256-568B-1

Query Match 98.1%; Score 20.6; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
|||||

RESULT 3
US-09-038-369B-1
; Sequence 1, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,369B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992

; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr-98"
US-09-038-369B-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 4

US-09-378-900A-1
; Sequence 1, Application US/09378900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr98"
US-09-378-900A-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 5

US-09-899-044-1
; Sequence 1, Application US/09899044
; Patent No. 6548244
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,044
; FILING DATE: 06-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0

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;
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-899-044-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 6
US-09-899-302-1
; Sequence 1, Application US/09899302
; Patent No. 6887985
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
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;
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr98"
US-09-899-302-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 7
US-09-899-082B-1
; Sequence 1, Application US/09899082B
; Patent No. 6891026
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Process for typing of HCV isolates
; FILE REFERENCE: 2551-111
; CURRENT APPLICATION NUMBER: US/09/899,082B
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 09/378,900
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 09/044,665
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/256,568
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: PCT/EP93/03325
; PRIOR FILING DATE: 1993-11-26
; PRIOR APPLICATION NUMBER: EP92403222
; PRIOR FILING DATE: 1992-11-27
; PRIOR APPLICATION NUMBER: EP93402129
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: HcPr98
US-09-899-082B-1
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Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 8

US-08-474-700B-2/c
; Sequence 2, Application US/08474700B
; Patent No. 6001990
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; APPLICANT: Moradpour, Darius
; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,700B
; FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,382
; FILING DATE: 10 May 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/279001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-474-700B-2

Query Match 98.1%; Score 20.6; DB 3; Length 28;
Best Local Similarity 95.2%; Pred. No. 0.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
Db 23 CCCTGTGAGGAAGTCTGTCT 3

RESULT 9

US-08-474-700B-29
; Sequence 29, Application US/08474700B
; Patent No. 6001990
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; APPLICANT: Moradpour, Darius
; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C

TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,700B
; FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,382
; FILING DATE: 10 May 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/279001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-474-700B-29

Query Match 98.1%; Score 20.6; DB 3; Length 28;
Best Local Similarity 95.2%; Pred. No. 0.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
Db 6 CCCTGTGAGGAAGTCTGTCT 26

RESULT 10

PCT-US95-05812-2/c
; Sequence 2, Application PC/TUS9505812
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; TITLE OF INVENTION: ANTISENSE INHIBITION OF
; TITLE OF INVENTION: HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05812
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,382
; FILING DATE: 10 May 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00786/221001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US95-05812-2

Query Match 98.1%; Score 20.6; DB 6; Length 28;
 Best Local Similarity 95.2%; Pred. No. 0.3;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 DB 23 CCCTGTGAGGAAGTCTGTCT 3

RESULT 11
 PCT-US95-05812-29
 ; Sequence 29, Application PC/TUS9505812
 ; GENERAL INFORMATION:
 ; APPLICANT: Wakita, Takaji
 ; TITLE OF INVENTION: ANTISENSE INHIBITION OF
 ; HEPATITIS C VIRUS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/05812
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/240,382
 ; FILING DATE: 10 May 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00786/221001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; PCT-US95-05812-29

Query Match 98.1%; Score 20.6; DB 6; Length 28;
 Best Local Similarity 95.2%; Pred. No. 0.3;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 DB 6 CCCTGTGAGGAAGTCTGTCT 26
 RESULT 12
 US-08-690-495-22/c
 ; Sequence 22, Application US/08690495
 ; Patent No. 5876924
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, David Y., Brandwein, Margaret
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
 ; HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10112-0228
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: FASSEQ Version #1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/690,495
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MacLeod, Janet M.
 ; REGISTRATION NUMBER: 35,263
 ; REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-408-2597
 ; TELEFAX: 212-765-2519
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..45
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US-08-690-495-22

Query Match 98.1%; Score 20.6; DB 2; Length 45;
 Best Local Similarity 95.2%; Pred. No. 0.32;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 13
 US-08-690-494-22/c
 ; Sequence 22, Application US/08690494
 ; Patent No. 5942391
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, David Y., Brandwein, Margaret
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
 ; HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA

ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PassSEQ Version #1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,494
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacLeod, Janet M.
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B
TELEPHONE: 212-408-2597
TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..45
US-08-690-494-22

Query Match 98.1%; Score 20.6; DB 2; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 14

US-09-299-217-22/c
Sequence 22, Application US/09299217
Patent No. 6569647

GENERAL INFORMATION:

APPLICANT: Zhang, David Y., Brandwein, Margaret
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10112-0228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PassSEQ Version #1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/299,217

FILING DATE: 23-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/690,494

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacLeod, Janet M.

REGISTRATION NUMBER: 35,263

REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-408-2597

TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..45
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-299-217-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 15

US-09-728-265-22/c
Sequence 22, Application US/09728265
Patent No. 6593086

GENERAL INFORMATION:

APPLICANT: Zhang, David Y.

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:

TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stroock & Stroock & Lavan

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10038

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/728,265

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Pokotilow, Steven B

REGISTRATION NUMBER: 26,405

REFERENCE/DOCKET NUMBER: Old 29545APCT/USA-B // New 251305/0018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212806-6663

TELEFAX: 2128066006

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..45

US-09-728-265-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 31 CCCTGTGAGGAAGTCTGTCT 11

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RESULT 16
US-10-309-438-22/c
; Sequence 22, Application US/10309438
; Patent No. 6855523
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Brandwein, Margaret
; APPLICANT: Hsuih, Terence C.H.
; TITLE OF INVENTION: Nucleic Acid Amplification Method: Ramification-extension
; TITLE OF INVENTION: amplification method (RAM)
; FILE REFERENCE: 251305/0031
; CURRENT APPLICATION NUMBER: US/10/309,438
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 09/299,217
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 08/690,494
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: US 08/596,331
; PRIOR FILING DATE: 1996-05-20
; PRIOR APPLICATION NUMBER: PCT/US95/07671
; PRIOR FILING DATE: 1995-06-14
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-309-438-22

Query Match          98.1%; Score 20.6; DB 3; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 17
PCT-US95-07671-22/c
; Sequence 22, Application PC/TUS9507671
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: LIGATION-DEPENDENT AMPLIFICATION FOR THE
; TITLE OF INVENTION: DETECTION OF INFECTIOUS PATHOGENS AND ABNORMAL GENES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07671
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: 29545-A-PCT
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 212-408-2626
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..45
PCT-US95-07671-22

Query Match          98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 18
US-09-798-641-22/c
; Sequence 22, Application US/09798641
; Patent No. RE38442
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y., Brandwein, Margaret
; TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PasSeq Version #1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/798,641
; FILING DATE: 02-Mar-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,495
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M.
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2597
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..45
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-798-641-22

Query Match          98.1%; Score 20.6; DB 8; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;

```


Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
|||||
Db 31 CCCTGTGAGGAACCTACTGTCT 11

RESULT 19

US-08-356-287-31
; Sequence 31, Application US/08356287
; Patent No. 5686272
; GENERAL INFORMATION:
; APPLICANT: Ronald L. Marshall
; APPLICANT: John J. Carrino
; APPLICANT: Joann Sustachek
; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING
; THE LIGASE CHAIN REACTION
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,287
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,543
; FILING DATE: 29 MAY 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul D. Yaegeer
; REGISTRATION NUMBER: 37,477
; REFERENCE/DOCKET NUMBER: 5172.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-2341
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

US-08-356-287-31

Query Match 98.1%; Score 20.6; DB 2; Length 51;
Best Local Similarity 95.2%; Pred. No. 0.33;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
|||||
Db 16 CCCTGTGAGGAACCTACTGTCT 36

RESULT 20

PCT-US93-04863-31
; Sequence 31, Application PC/TUS9304863
; GENERAL INFORMATION:
; APPLICANT: Ronald L. Marshall
; APPLICANT: John J. Carrino
; APPLICANT: Joann C. Sustachek
; APPLICANT: ABBOTT LABORATORIES
; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
; USING THE LIGASE CHAIN REACTION
; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04863
; FILING DATE: 19930524
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,543
; FILING DATE: 29 MAY 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5172.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
PCT-US93-04863-31

Query Match 98.1%; Score 20.6; DB 6; Length 51;
Best Local Similarity 95.2%; Pred. No. 0.33;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
|||||
Db 16 CCCTGTGAGGAACCTACTGTCT 36

RESULT 21

US-08-474-700B-42/c
; Sequence 42, Application US/08474700B
; Patent No. 6001990
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; APPLICANT: Moradpour, Darius
; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
; VIRUS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,700B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,382
; FILING DATE: 10 May 1994

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/279001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-474-700B-42

Query Match 98.1%; Score 20.6; DB 3; Length 67;
Best Local Similarity 95.2%; Pred. No. 0.35;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 25 CCCTGTGAGGAAGTCTGTCT 5

RESULT 22
US-08-474-700B-41/c
Sequence 41, Application US/08474700B
Patent No. 6001990
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Wakita, Takaji
APPLICANT: Moradpour, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,700B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/279001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-474-700B-41

Query Match 98.1%; Score 20.6; DB 3; Length 155;

Best Local Similarity 95.2%; Pred. No. 0.41;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 113 CCCTGTGAGGAAGTCTGTCT 93

RESULT 23
US-08-335-595-1
Sequence 1, Application US/08335595
Patent No. 5914228
GENERAL INFORMATION:
APPLICANT: VIERLING, JOHN M
APPLICANT: HU, KE-QIN
TITLE OF INVENTION: DIRECT DETECTION OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 611 WEST 6TH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,595
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/175,473
FILING DATE:
APPLICATION NUMBER: US/07/758,862
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SCHNEIDER, CAROL A
REGISTRATION NUMBER: 34,923
REFERENCE/DOCKET NUMBER: 194/285
TELEPHONE: 213-489-1600
TELEFAX: 213-955-0440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-335-595-1

Query Match 98.1%; Score 20.6; DB 2; Length 242;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 20 CCCTGTGAGGAAGTCTGTCT 40

RESULT 24
US-08-474-700B-40/c
Sequence 40, Application US/08474700B
Patent No. 6001990
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Wakita, Takaji
APPLICANT: Moradpour, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
TITLE OF INVENTION: VIRUS

; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.1)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,700B
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/240,382
 ; FILING DATE: 10 May 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 00786/279001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 260 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-474-700B-40

Query Match 98.1%; Score 20.6; DB 3; Length 260;
 Best Local Similarity 95.2%; Pred. No. 0.45;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 DB 218 CCCTGTGAGGAAGTCTGTCT 198

RESULT 25
 US-09-899-082B-98
 ; Sequence 98, Application US/09899082B
 ; Patent No. 6891026
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Process for typing of HCV isolates
 ; FILE REFERENCE: 2551-111
 ; CURRENT APPLICATION NUMBER: US/09/899,082B
 ; CURRENT FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 09/378,900
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 09/044,665
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 08/256,568
 ; PRIOR FILING DATE: 1994-07-18
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325
 ; PRIOR FILING DATE: 1993-11-26
 ; PRIOR APPLICATION NUMBER: EP92403222
 ; PRIOR FILING DATE: 1992-11-27
 ; PRIOR APPLICATION NUMBER: EP93402129
 ; PRIOR FILING DATE: 1993-08-31
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 98
 ; LENGTH: 260
 ; TYPE: DNA
 ; ORGANISM: hepatitis C virus

; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Process for typing of HCV isolates
 ; FILE REFERENCE: 2551-111
 ; CURRENT APPLICATION NUMBER: US/09/899,082B
 ; CURRENT FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 09/378,900
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 09/044,665
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 08/256,568
 ; PRIOR FILING DATE: 1994-07-18
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325
 ; PRIOR FILING DATE: 1993-11-26
 ; PRIOR APPLICATION NUMBER: EP92403222
 ; PRIOR FILING DATE: 1992-11-27
 ; PRIOR APPLICATION NUMBER: EP93402129
 ; PRIOR FILING DATE: 1993-08-31
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 98
 ; LENGTH: 260
 ; TYPE: DNA
 ; ORGANISM: hepatitis C virus

US-09-899-082B-98
 Query Match 98.1%; Score 20.6; DB 3; Length 260;
 Best Local Similarity 95.2%; Pred. No. 0.45;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 DB 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 26
 US-09-899-082B-99
 ; Sequence 99, Application US/09899082B
 ; Patent No. 6891026
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Process for typing of HCV isolates
 ; FILE REFERENCE: 2551-111
 ; CURRENT APPLICATION NUMBER: US/09/899,082B
 ; CURRENT FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 09/378,900
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 09/044,665
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 08/256,568
 ; PRIOR FILING DATE: 1994-07-18
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325
 ; PRIOR FILING DATE: 1993-11-26
 ; PRIOR APPLICATION NUMBER: EP92403222
 ; PRIOR FILING DATE: 1992-11-27
 ; PRIOR APPLICATION NUMBER: EP93402129
 ; PRIOR FILING DATE: 1993-08-31
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 99
 ; LENGTH: 260
 ; TYPE: DNA
 ; ORGANISM: hepatitis C virus
 ; US-09-899-082B-99

Query Match 98.1%; Score 20.6; DB 3; Length 260;
 Best Local Similarity 95.2%; Pred. No. 0.45;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 DB 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 27
 US-09-899-082B-100
 ; Sequence 100, Application US/09899082B
 ; Patent No. 6891026
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: Process for typing of HCV isolates
 ; FILE REFERENCE: 2551-111
 ; CURRENT APPLICATION NUMBER: US/09/899,082B
 ; CURRENT FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 09/378,900
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 09/044,665
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 08/256,568
 ; PRIOR FILING DATE: 1994-07-18
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325
 ; PRIOR FILING DATE: 1993-11-26
 ; PRIOR APPLICATION NUMBER: EP92403222
 ; PRIOR FILING DATE: 1992-11-27
 ; PRIOR APPLICATION NUMBER: EP93402129
 ; PRIOR FILING DATE: 1993-08-31
 ; NUMBER OF SEQ ID NOS: 128

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 260
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-899-082B-100

Query Match          98.1%; Score 20.6; DB 3; Length 260;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
Db 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 28
US-09-899-082B-101
; Sequence 101, Application US/09899082B
; Patent No. 6891026
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Process for typing of HCV isolates
; FILE REFERENCE: 2551-111
; CURRENT APPLICATION NUMBER: US/09/899,082B
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 09/378,900
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 09/044,665
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/256,568
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: PCT/EP93/03325
; PRIOR FILING DATE: 1993-11-26
; PRIOR APPLICATION NUMBER: EP92403222
; PRIOR FILING DATE: 1992-11-27
; PRIOR APPLICATION NUMBER: EP93402129
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 260
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-899-082B-101

Query Match          98.1%; Score 20.6; DB 3; Length 260;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
Db 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 29
US-08-332-616A-1
; Sequence 1, Application US/08332616A
; Patent No. 5620852
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; APPLICANT: CIMINO, GEORGE
; APPLICANT: ZHU, YU SHENG
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,921
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 305 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-317-220-1

Query Match 98.1%; Score 20.6; DB 2; Length 305;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 31
 US-08-444-818-108
 ; Sequence 108, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-108

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 32
 US-08-444-818-109/c
 ; Sequence 109, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 109:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-109

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 290 CCCTGTGAGGAAGTCTGTCT 270

RESULT 33
 US-08-444-818-110
 ; Sequence 110, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-108

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

Db 19 CCCTGTGAGGAAGTCTGTCT 39

RESULT 32
 US-08-444-818-109/c
 ; Sequence 109, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 109:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ANTI-SENSE: YES
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-109

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 290 CCCTGTGAGGAAGTCTGTCT 270

RESULT 33
 US-08-444-818-110
 ; Sequence 110, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 109:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ANTI-SENSE: YES
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-109

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 290 CCCTGTGAGGAAGTCTGTCT 270

RESULT 33
 US-08-444-818-110
 ; Sequence 110, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 109:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ANTI-SENSE: YES
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-109

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 290 CCCTGTGAGGAAGTCTGTCT 270

RESULT 33
 US-08-444-818-110
 ; Sequence 110, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: 18g
 ; US-08-444-818-108

Query Match 98.1%; Score 20.6; DB 3; Length 308;
 Best Local Similarity 95.2%; Pred. No. 0.47;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 18g
FEATURE:
NAME/KEY: CDS
LOCATION: 2..55
US-08-444-818-112

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 19 CCTGTGAGGAAGTCTGTCT 39
|||||

RESULT 35
US-08-444-818-114
Sequence 114, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 18g

COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 18g
FEATURE:
NAME/KEY: CDS
LOCATION: 1..72
US-08-444-818-110

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 19 CCTGTGAGGAAGTCTGTCT 39
|||||

RESULT 34
US-08-444-818-112
Sequence 112, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:

FEATURE:
NAME/KEY: CDS
LOCATION: 72..116
US-08-444-818-114

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
DB 19 CCTGTGAGGAAGTCTGTCT 39

RESULT 36

US-08-444-818-116
Sequence 116, Application US/08444818
Patent No. 6150087

GENERAL INFORMATION:

APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA

ZIP: 94608-2916
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,818
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,590

FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Harbin, Alisa A.

REGISTRATION NUMBER: 33,895

REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)359-3876

TELEFAX: (508)359-3885

INFORMATION FOR SEQ ID NO: 116:

SEQUENCE CHARACTERISTICS:

LENGTH: 308 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: 18g

FEATURE:

NAME/KEY: CDS

LOCATION: 191..226

US-08-444-818-116

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
DB 19 CCTGTGAGGAAGTCTGTCT 39

RESULT 37

US-08-444-818-118
Sequence 118, Application US/08444818
Patent No. 6150087

GENERAL INFORMATION:

APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,818

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,590

FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Harbin, Alisa A.

REGISTRATION NUMBER: 33,895

REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)359-3876

TELEFAX: (508)359-3885

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:

LENGTH: 308 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: 18g

FEATURE:

NAME/KEY: CDS

LOCATION: 276..308

US-08-444-818-118

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
DB 19 CCTGTGAGGAAGTCTGTCT 39

RESULT 38

US-08-470-426B-1

Sequence 1, Application US/08470426B

Patent No. 5856458

GENERAL INFORMATION:

APPLICANT: Okamoto, Hiroaki

APPLICANT: Nakamura, Tetsuo

TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR

APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B

HEPATITIS VIRUS

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,

L.L.P.

STREET: 1850 M Street, N.W., Suite 800

CITY: Washington

```
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,426B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-153402
; FILING DATE: 12-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillacher, Robert G.
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/59-47083.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2811
; TELEFAX: (202) 659-1462
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-470-426B-1

Query Match 98.1%; Score 20.6; DB 2; Length 324;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 26 CCCTGTGAGGAAGTCTGTCT 46

RESULT 39
US-08-470-426B-15
; Sequence 15, Application US/08470426B
; Patent No. 5856458
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Hiroaki
; APPLICANT: Nakamura, Tetsuo
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
; TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
; TITLE OF INVENTION: HEPATITIS VIRUS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beveridge, DeGrandi, Weillacher & Young,
; ADDRESSEE: L.L.P.
; STREET: 1850 M Street, N.W., Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,426B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-153402
; FILING DATE: 12-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillacher, Robert G.
```

```
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/59-47083.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2811
; TELEFAX: (202) 659-1462
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-470-426B-15

Query Match 98.1%; Score 20.6; DB 2; Length 324;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 26 CCCTGTGAGGAAGTCTGTCT 46

RESULT 40
US-08-440-209-1
; Sequence 1, Application US/08440209
; Patent No. 5922857
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,209
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,895
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ns5hev1
; US-08-440-209-1
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Query Match 98.1%; Score 20.6; DB 2; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
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DB 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 41

US-08-854-531-4
; Sequence 4, Application US/08854531
; Patent No. 6025341
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Tokushige, Katsutoshi
; APPLICANT: Wakita, Takaji
; TITLE OF INVENTION: CHIMERIC HEPATITIS B/HEPATITIS C VIRUS VACCINE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6025341ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,531
; FILING DATE: Herewith

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: APOL-0214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-854-531-4

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
DB 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 42

US-08-439-996-1
; Sequence 1, Application US/08439996
; Patent No. 6057093
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,996
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,895A
; FILING DATE:
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janluk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
; LENGTH: 341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ns5hcv1
US-08-439-996-1

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
DB 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 43

US-09-014-416-47
; Sequence 47, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-47

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 44
US-09-014-416-48
; Sequence 48, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-48

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 45
US-09-014-416-49
; Sequence 49, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-49

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 46
US-08-869-380-4
; Sequence 4, Application US/08869380
; Patent No. 6235888
; GENERAL INFORMATION:
; APPLICANT: Pachuk, Catherine J.
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; APPLICANT: Zurawski, Jr., Vincent R.
; APPLICANT: Coney, Leslie R.
; TITLE OF INVENTION: Hepatitis C Virus Vaccine
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6235888ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,248
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: APOL-0189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-869-380-4

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 47
US-09-814-351-3
; Sequence 3, Application US/09814351
; Patent No. 6692736
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' UTR region of HCV
US-09-814-351-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

RESULT 48

US-09-814-292-44
; Sequence 44, Application US/09814292
; Patent No. 6852528
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Zhang, Hong
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 348022001500
; CURRENT APPLICATION NUMBER: US/09/814,292
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' UTR region of HCV
US-09-814-292-44

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

RESULT 49

US-09-814-357-3
; Sequence 3, Application US/09814357
; Patent No. 6911200
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

; LENGTH: 341
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' UTR region of HCV
US-09-814-357-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

RESULT 50

US-10-259-275-35
; Sequence 35, Application US/10259275
; Patent No. 6921634
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley M.
; APPLICANT: Yi, Minkyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0120
; CURRENT APPLICATION NUMBER: US/10/259,275
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 09/747,419
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/325,236
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/338,123
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 35
; LENGTH: 341
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of 5' NTR
US-10-259-275-35

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

Search completed: January 27, 2006, 07:08:53
Job time : 73.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:37:30 ; Search time 348.5 Seconds
(without alignments)
498.298 Million cell updates/sec

Title: US-10-070-415A-37_COPY_410_430

Perfect score: 21
Sequence: 1 gcaagtgctgtagtgccggg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	95.2	581	7	US-10-070-415A-18
5	20	95.2	581	7	US-10-070-415A-19
6	19.4	92.4	581	3	US-09-813-031-1
7	19.4	92.4	581	3	US-09-813-031-2
8	19.4	92.4	581	3	US-09-813-031-3
9	19.4	92.4	581	3	US-09-813-031-4
10	19.4	92.4	581	3	US-09-813-990A-1
11	19.4	92.4	581	3	US-09-813-990A-2
12	19.4	92.4	581	3	US-09-813-990A-3
13	19.4	92.4	581	3	US-09-813-990A-4
14	19.4	92.4	581	7	US-10-070-415A-38
15	19.4	92.4	581	7	US-10-070-415A-39
16	19.4	92.4	581	7	US-10-070-415A-40
17	19.4	92.4	581	9	US-10-633-659-1
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19	19.4	92.4	581	9	US-10-633-659-3
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22	19.4	92.4	5376	8	US-10-492-396-7
23	17.8	84.8	752	7	US-10-424-599-60215

24	17.8	84.8	5981	6	US-10-311-455-2165	Sequence 2165, Ap
25	17	81.0	3302	3	US-09-968-007A-992	Sequence 992, App
26	17	81.0	3302	7	US-10-755-889-357	Sequence 357, App
27	17	81.0	3302	9	US-10-843-641A-7462	Sequence 7462, Ap
28	17	81.0	3302	9	US-10-887-553A-335	Sequence 335, App
29	17	81.0	3579	5	US-10-198-846-11469	Sequence 11469, A
30	16.8	80.0	565	9	US-10-972-079-13406	Sequence 13406, A
31	16.8	80.0	595	9	US-10-972-079-13405	Sequence 13405, A
32	16.8	80.0	954	9	US-10-450-763-29555	Sequence 29555, A
33	16.8	80.0	1840	9	US-10-450-763-17672	Sequence 17672, A
34	16.8	80.0	2178	9	US-10-450-763-17668	Sequence 17668, A
35	16.8	80.0	2179	9	US-10-450-763-25501	Sequence 25501, A
36	16.8	80.0	2250	9	US-10-450-763-29558	Sequence 29558, A
37	16.8	80.0	2830	9	US-10-450-763-29562	Sequence 29562, A
38	16.8	80.0	3039	9	US-10-450-763-25465	Sequence 25465, A
39	16.8	80.0	3039	9	US-10-450-763-29044	Sequence 29044, A
40	16.8	80.0	3039	9	US-10-450-763-29143	Sequence 29143, A
41	16.8	80.0	3355	9	US-10-450-763-21560	Sequence 21560, A
42	16.8	80.0	4134	3	US-09-815-274-6287	Sequence 6287, Ap
43	16.8	80.0	4134	6	US-10-287-274-296	Sequence 296, App
44	16.8	80.0	4134	7	US-10-282-122A-6547	Sequence 6547, Ap
45	16.8	80.0	4194	7	US-10-282-122A-6875	Sequence 6875, Ap
46	16.8	80.0	4236	7	US-10-282-122A-6876	Sequence 6876, Ap
47	16.8	80.0	5471	9	US-10-450-763-26014	Sequence 26014, A
48	16.8	80.0	5519	5	US-10-114-170-226	Sequence 226, App
49	16.8	80.0	9072	2	US-08-781-986A-45	Sequence 45, Appl
50	16.8	80.0	9072	7	US-10-329-624-45	Sequence 45, Appl
51	16.2	77.1	520	5	US-10-027-632-287754	Sequence 287754, A
52	16.2	77.1	520	6	US-10-027-632-287754	Sequence 287754, A
53	16.2	77.1	590	4	US-09-925-065A-545841	Sequence 545841, A
54	16.2	77.1	610	4	US-09-925-065A-630591	Sequence 630591, A
55	16.2	77.1	760	5	US-10-027-632-145547	Sequence 145547, A
56	16.2	77.1	760	6	US-10-027-632-145547	Sequence 145547, A
57	16.2	77.1	786	8	US-10-435-115-67484	Sequence 67484, A
58	16.2	77.1	945	9	US-10-511-278-89	Sequence 89, Appl
59	16.2	77.1	948	8	US-10-774-355A-126	Sequence 126, App
60	16.2	77.1	954	6	US-10-029-386-24933	Sequence 24933, A
61	16.2	77.1	989	6	US-10-024-212-39	Sequence 39, Appl
62	16.2	77.1	995	6	US-10-025-806-31	Sequence 31, Appl
63	16.2	77.1	1110	6	US-10-411-224-11	Sequence 11, Appl
64	16.2	77.1	1110	6	US-10-047-021-11	Sequence 11, Appl
65	16.2	77.1	1110	9	US-10-970-493-11	Sequence 11, Appl
66	16.2	77.1	1146	9	US-10-450-763-7562	Sequence 7562, Ap
67	16.2	77.1	1282	6	US-10-305-720-1413	Sequence 1413, Ap
68	16.2	77.1	1324	7	US-10-260-238-1698	Sequence 1698, Ap
69	16.2	77.1	1481	8	US-10-739-930-5282	Sequence 5282, Ap
70	16.2	77.1	1668	7	US-10-425-114-2656	Sequence 2656, Ap
71	16.2	77.1	1751	8	US-10-425-115-1393	Sequence 1393, Ap
72	16.2	77.1	2746	8	US-10-739-930-4188	Sequence 4188, Ap
73	16.2	77.1	3009	6	US-10-369-493-25065	Sequence 25065, A
74	16.2	77.1	3280	7	US-10-437-963-73692	Sequence 73692, A
75	16.2	77.1	3492	7	US-10-437-963-93329	Sequence 93329, A
76	16.2	77.1	3519	9	US-10-887-553A-684	Sequence 684, App
77	16.2	77.1	11771	9	US-10-415-620-1	Sequence 1, Appl
78	16.2	77.1	25760	3	US-09-999-121-13	Sequence 13, Appl
79	16.2	77.1	42823	8	US-10-643-801-18	Sequence 18, Appl
80	16.2	77.1	52799	7	US-10-322-281-630	Sequence 630, App
81	16.2	77.1	347001	7	US-10-319-908-16	Sequence 16, Appl
82	16	76.2	25	8	US-10-719-900-929123	Sequence 929123, A
83	15.8	75.2	201	8	US-10-719-993-17805	Sequence 17805, A
84	15.8	75.2	236	3	US-09-796-692-6242	Sequence 6242, Ap
85	15.8	75.2	236	5	US-10-040-862-6242	Sequence 6242, Ap
86	15.8	75.2	236	6	US-10-057-475B-6242	Sequence 6242, Ap
87	15.8	75.2	236	6	US-10-154-884B-6242	Sequence 6242, Ap
88	15.8	75.2	236	7	US-10-784-324-6242	Sequence 6242, Ap
89	15.8	75.2	286	7	US-10-424-599-133670	Sequence 133670, A
90	15.8	75.2	340	3	US-09-867-701-4147	Sequence 4147, Ap
91	15.8	75.2	399	4	US-09-925-065A-239953	Sequence 239953, A
92	15.8	75.2	543	3	US-09-933-561-9	Sequence 9, Appl
93	15.8	75.2	559	9	US-10-487-901-5512	Sequence 5512, Ap
94	15.8	75.2	600	9	US-10-972-079-34586	Sequence 34586, A
95	15.8	75.2	661	9	US-10-487-901-5513	Sequence 5513, Ap
96	15.8	75.2	681	7	US-10-437-963-33361	Sequence 33361, A

97 15.8 75.2 696 5 US-10-027-632-136957 Sequence 136957,
 98 15.8 75.2 696 6 US-10-027-632-136957 Sequence 136957,
 99 15.8 75.2 777 7 US-10-260-238-4421 Sequence 4421, Ap
 c 100 15.8 75.2 1028 7 US-10-437-963-3037 Sequence 3037, Ap

ALIGNMENTS

RESULT 1
 US-10-070-415A-37
 ; Sequence 37, Application US/10070415A
 ; Publication No. US20040043379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HASHIMOTO, Koji
 ; APPLICANT: ASHIMOTO, Michie
 ; APPLICANT: MISHIRO, Shunji
 ; APPLICANT: OOTA, Yasuhiko
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
 ; FILE REFERENCE: 220633US2SRDPCT
 ; CURRENT APPLICATION NUMBER: US/10/070,415A
 ; CURRENT FILING DATE: 2003-07-23
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: JP 2001-090053
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: JP 2001-284112
 ; PRIOR FILING DATE: 2001-09-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (455)..(455)
 ; OTHER INFORMATION: n is one nucleotide selected from a, g, c, or t
 US-10-070-415A-37

Query Match 100.0%; Score 21; DB 7; Length 581;
 Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
 |||||
 Db 410 GCAAGTGCTGTAGTGGCGGG 430

RESULT 2
 US-10-070-415A-16
 ; Sequence 16, Application US/10070415A
 ; Publication No. US20040043379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HASHIMOTO, Koji
 ; APPLICANT: ASHIMOTO, Michie
 ; APPLICANT: MISHIRO, Shunji
 ; APPLICANT: OOTA, Yasuhiko
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
 ; FILE REFERENCE: 220633US2SRDPCT
 ; CURRENT APPLICATION NUMBER: US/10/070,415A
 ; CURRENT FILING DATE: 2003-07-23
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: JP 2001-090053
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: JP 2001-284112
 ; PRIOR FILING DATE: 2001-09-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 581
 ; TYPE: DNA

; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (420)..(420)
 ; OTHER INFORMATION: n is one nucleotide selected from a, g, c, or t
 US-10-070-415A-16

Query Match 95.2%; Score 20; DB 7; Length 581;
 Best Local Similarity 95.2%; Pred. No. 13;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
 |||||
 Db 410 GCAAGTGCTGTAGTGGCGGG 430

RESULT 3
 US-10-070-415A-17
 ; Sequence 17, Application US/10070415A
 ; Publication No. US20040043379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HASHIMOTO, Koji
 ; APPLICANT: ASHIMOTO, Michie
 ; APPLICANT: MISHIRO, Shunji
 ; APPLICANT: OOTA, Yasuhiko
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
 ; FILE REFERENCE: 220633US2SRDPCT
 ; CURRENT APPLICATION NUMBER: US/10/070,415A
 ; CURRENT FILING DATE: 2003-07-23
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: JP 2001-090053
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: JP 2001-284112
 ; PRIOR FILING DATE: 2001-09-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 17
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (420)..(420)
 ; OTHER INFORMATION: n is any nucleotide selected from a, g, c, or t
 US-10-070-415A-17

Query Match 95.2%; Score 20; DB 7; Length 581;
 Best Local Similarity 95.2%; Pred. No. 13;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
 |||||
 Db 410 GCAAGTGCTGTAGTGGCGGG 430

RESULT 4
 US-10-070-415A-18
 ; Sequence 18, Application US/10070415A
 ; Publication No. US20040043379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HASHIMOTO, Koji
 ; APPLICANT: ASHIMOTO, Michie
 ; APPLICANT: MISHIRO, Shunji
 ; APPLICANT: OOTA, Yasuhiko
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
 ; FILE REFERENCE: 220633US2SRDPCT
 ; CURRENT APPLICATION NUMBER: US/10/070,415A
 ; CURRENT FILING DATE: 2003-07-23
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: JP 2001-090053
 ; PRIOR FILING DATE: 2001-03-27

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; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (420)..(420)
; OTHER INFORMATION: n is any nucleotide selected from a, g, c, or t
US-10-070-415A-18

Query Match          95.2%; Score 20; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 5
US-10-070-415A-19
; Sequence 19, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, Koji
; APPLICANT: ASHIMOTO, Michie
; APPLICANT: MISHIRO, Shunji
; APPLICANT: OOTA, Yasuhiko
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
; FILE REFERENCE: 220633US2SRDPCT
; CURRENT APPLICATION NUMBER: US/10/070,415A
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: PCT/JP02/02030
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: JP 2001-090053
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (420)..(420)
; OTHER INFORMATION: n is any nucleotide selected from a, g, c, or t
US-10-070-415A-19

Query Match          95.2%; Score 20; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 6
US-09-813-031-1
; Sequence 1, Application US/09813031
; Patent No. US20020048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058USOSRD
; CURRENT APPLICATION NUMBER: US/09/813,031

```

```

; TITLE OF INVENTION: INTERFERON THERAPY
; FILE REFERENCE: 205058USOSRD
; CURRENT APPLICATION NUMBER: US/09/813,031
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-031-1

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 7
US-09-813-031-2
; Sequence 2, Application US/09813031
; Patent No. US20020048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058USOSRD
; CURRENT APPLICATION NUMBER: US/09/813,031
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-031-2

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 8
US-09-813-031-3
; Sequence 3, Application US/09813031
; Patent No. US20020048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058USOSRD
; CURRENT APPLICATION NUMBER: US/09/813,031

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; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: JP2000-080955
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: JP2001-062372
 ; PRIOR FILING DATE: 2001-03-06
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-031-3

Query Match 92.4%; Score 19.4; DB 3; Length 581;
 Best Local Similarity 95.2%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21
 |||||
 Db 410 GCAAGTGCTGMAGTGGGG 430

RESULT 9
 US-09-813-031-4
 ; Sequence 4, Application US/09813031
 ; Patent No. US2002048758A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hijikata, Minako
 ; APPLICANT: Mishiro, Shunji
 ; APPLICANT: Oota, Yasuhiko
 ; APPLICANT: Hashimoto, Koji
 ; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
 ; TITLE OF INVENTION: INTERFERON THERAPY
 ; FILE REFERENCE: 205058US0SRD
 ; CURRENT APPLICATION NUMBER: US/09/813,031
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: JP2000-080955
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: JP2001-062372
 ; PRIOR FILING DATE: 2001-03-06
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-031-4

Query Match 92.4%; Score 19.4; DB 3; Length 581;
 Best Local Similarity 95.2%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21
 |||||
 Db 410 GCAAGTGCTGMAGTGGGG 430

RESULT 10
 US-09-813-990A-1
 ; Sequence 1, Application US/09813990A
 ; Patent No. US20020127558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HIJIKATA, MINAKO
 ; APPLICANT: MISHIRO, SHUNJI
 ; APPLICANT: OOTA, YASUHIKO
 ; APPLICANT: HASHIMOTO, KOJI
 ; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
 ; FILE REFERENCE: 205057US0SRD
 ; CURRENT APPLICATION NUMBER: US/09/813,990A
 ; CURRENT FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: JP2000-080955
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: JP2001-062371

; PRIOR FILING DATE: 2001-03-06
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-990A-1

Query Match 92.4%; Score 19.4; DB 3; Length 581;
 Best Local Similarity 95.2%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21
 |||||
 Db 410 GCAAGTGCTGMAGTGGGG 430

RESULT 11
 US-09-813-990A-2
 ; Sequence 2, Application US/09813990A
 ; Patent No. US20020127558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HIJIKATA, MINAKO
 ; APPLICANT: MISHIRO, SHUNJI
 ; APPLICANT: OOTA, YASUHIKO
 ; APPLICANT: HASHIMOTO, KOJI
 ; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
 ; FILE REFERENCE: 205057US0SRD
 ; CURRENT APPLICATION NUMBER: US/09/813,990A
 ; CURRENT FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: JP2000-080955
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: JP2001-062371
 ; PRIOR FILING DATE: 2001-03-06
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-990A-2

Query Match 92.4%; Score 19.4; DB 3; Length 581;
 Best Local Similarity 95.2%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21
 |||||
 Db 410 GCAAGTGCTGMAGTGGGG 430

RESULT 12
 US-09-813-990A-3
 ; Sequence 3, Application US/09813990A
 ; Patent No. US20020127558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HIJIKATA, MINAKO
 ; APPLICANT: MISHIRO, SHUNJI
 ; APPLICANT: OOTA, YASUHIKO
 ; APPLICANT: HASHIMOTO, KOJI
 ; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
 ; FILE REFERENCE: 205057US0SRD
 ; CURRENT APPLICATION NUMBER: US/09/813,990A
 ; CURRENT FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: JP2000-080955
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: JP2001-062371
 ; PRIOR FILING DATE: 2001-03-06
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 581

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-3

Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 13

US-09-813-990A-4
; Sequence 4, Application US/09813990A
; Patent No. US20020127558A1
; GENERAL INFORMATION:
; APPLICANT: HJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US05RD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; TYPE: DNA
; LENGTH: 581
; ORGANISM: Homo sapiens
US-09-813-990A-4

Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 14

US-10-070-415A-38
; Sequence 38, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, KOJI
; APPLICANT: ASHIMOTO, Michie
; APPLICANT: MISHIRO, Shunji
; APPLICANT: OOTA, Yasuhiko
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
; FILE REFERENCE: 220633US2SRDPT
; CURRENT APPLICATION NUMBER: US/10/070,415A
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: PCT/JP02/02030
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: JP 2001-090053
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc.feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is one nucleotide selected from a, g, c, or t
US-10-070-415A-38

Query Match 92.4%; Score 19.4; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 15

US-10-070-415A-39
; Sequence 39, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, KOJI
; APPLICANT: ASHIMOTO, Michie
; APPLICANT: MISHIRO, Shunji
; APPLICANT: OOTA, Yasuhiko
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
; FILE REFERENCE: 220633US2SRDPT
; CURRENT APPLICATION NUMBER: US/10/070,415A
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: PCT/JP02/02030
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: JP 2001-090053
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
US-10-070-415A-39

Query Match 92.4%; Score 19.4; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 16

US-10-070-415A-40
; Sequence 40, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, KOJI
; APPLICANT: ASHIMOTO, Michie
; APPLICANT: MISHIRO, Shunji
; APPLICANT: OOTA, Yasuhiko
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
; FILE REFERENCE: 220633US2SRDPT
; CURRENT APPLICATION NUMBER: US/10/070,415A
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: PCT/JP02/02030
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: JP 2001-090053
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18

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; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
US-10-070-415A-40

Query Match          92.4%; Score 19.4; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   ||||| ||||| ||||| |||||
Db 410 GCAAGTGCTGAGGTGGGG 430

RESULT 17
US-10-633-659-1
; Sequence 1, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/813,031
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-1

Query Match          92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   ||||| ||||| ||||| |||||
Db 410 GCAAGTGCTGAGGTGGGG 430

RESULT 18
US-10-633-659-2
; Sequence 2, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/813,031
```

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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-2

Query Match          92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   ||||| ||||| ||||| |||||
Db 410 GCAAGTGCTGAGGTGGGG 430

RESULT 19
US-10-633-659-3
; Sequence 3, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/813,031
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-3

Query Match          92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   ||||| ||||| ||||| |||||
Db 410 GCAAGTGCTGAGGTGGGG 430

RESULT 20
US-10-633-659-4
; Sequence 4, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
```

; PRIOR APPLICATION NUMBER: US/09/813,031
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-4

Query Match 92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTTCGGGG 21
|||||
Db 410 GCAAGTCTGTAGTTCGGGG 430

RESULT 21

US-10-492-396-5
; Sequence 5, Application US/10492396
; Publication No. US20040209800A1
; GENERAL INFORMATION:
; APPLICANT: MUSHINSKI, J F
; APPLICANT: TREPEL, JANE B
; APPLICANT: HORISBERGER, MICHEL A
; APPLICANT: NGUYEN, PHUONGMAI
; APPLICANT: CHANG, KHANNA
; TITLE OF INVENTION: USE OF Mx GTPases IN THE PROGNOSIS AND TREATMENT OF CANCER
; FILE REFERENCE: 403025
; CURRENT APPLICATION NUMBER: US/10/492,396
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/33232
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/329,740
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-492-396-5

Query Match 92.4%; Score 19.4; DB 8; Length 2451;
Best Local Similarity 95.2%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTTCGGGG 21
|||||
Db 2398 GCAAGTCTGTAGTTCGGGG 2418

RESULT 22

US-10-492-396-7
; Sequence 7, Application US/10492396
; Publication No. US20040209800A1
; GENERAL INFORMATION:
; APPLICANT: MUSHINSKI, J F
; APPLICANT: TREPEL, JANE B
; APPLICANT: HORISBERGER, MICHEL A
; APPLICANT: NGUYEN, PHUONGMAI
; APPLICANT: CHANG, KHANNA
; TITLE OF INVENTION: USE OF Mx GTPases IN THE PROGNOSIS AND TREATMENT OF CANCER
; FILE REFERENCE: 403025
; CURRENT APPLICATION NUMBER: US/10/492,396
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/33232

; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/329,740
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5376
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-492-396-7

Query Match 92.4%; Score 19.4; DB 8; Length 5376;
Best Local Similarity 95.2%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTTCGGGG 21
|||||
Db 444 GCAAGTCTGTAGTTCGGGG 464

RESULT 23

US-10-424-599-60215
; Sequence 60215, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 60215
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(752)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25386C.1
US-10-424-599-60215

Query Match 84.8%; Score 17.8; DB 7; Length 752;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTTCGGGG 21
|||||
Db 615 GCAAGTCTGTAGTTCGGGG 635

RESULT 24

US-10-311-455-2165
; Sequence 2165, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02

```
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2165
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2165

Query Match      84.8%; Score 17.8; DB 6; Length 5981;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCAAGTCTAGTGC GGCGG 21
Db      4867  GTAAGTGTAGTGC GGCGG 4887

RESULT 25
US-09-968-007A-992/c
; Sequence 992, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 992
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-992

Query Match      81.0%; Score 17; DB 3; Length 3302;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GTGCTGTAGTGC GGCGG 21
Db      541  GTGCTGTAGTGC GGCGG 525

RESULT 26
US-10-755-889-357/c
; Sequence 357, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
```

```
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n=a,t,g or c
US-10-755-889-357

Query Match      81.0%; Score 17; DB 7; Length 3302;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GTGCTGTAGTGC GGCGG 21
Db      541  GTGCTGTAGTGC GGCGG 525

RESULT 27
US-10-843-641A-7462/c
; Sequence 7462, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7462
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(3302)
; OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-7462

Query Match      81.0%; Score 17; DB 9; Length 3302;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GTGCTGTAGTGC GGCGG 21
Db      541  GTGCTGTAGTGC GGCGG 525
```

RESULT 28

US-10-887-553A-335/c
; Sequence 335, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-335

Query Match 81.0%; Score 17; DB 9; Length 3302;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 541 GTGCTGTAGTGGCGGG 525

RESULT 29

US-10-198-846-11469/c
; Sequence 11469, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11469
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3559-3560, 3561, 3562, 3563, 3564, 3565, 3566, 3567, 3568,
; LOCATION: 3569, 3570, 3571, 3572, 3573, 3574, 3575, 3576, 3577, 3578,
; LOCATION: 3579
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11469

Query Match 81.0%; Score 17; DB 5; Length 3579;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 628 GTGCTGTAGTGGCGGG 612

RESULT 30

US-10-450-763-29555/c

; Sequence 29555, Application US/10450763

; Publication No. US20050196754A1

US-10-972-079-13406

; Sequence 13406, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BE
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13406
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Chicken 19866894217856_4
US-10-972-079-13406

Query Match 80.0%; Score 16.8; DB 9; Length 565;

Best Local Similarity 90.0%; Pred. No. 4.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 20

Db 486 GCAAGTGTCTAGTGGCGGG 505

RESULT 31

US-10-972-079-13405
; Sequence 13405, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BE
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13405
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Chicken 19866894217856_3
US-10-972-079-13405

Query Match 80.0%; Score 16.8; DB 9; Length 595;

Best Local Similarity 90.0%; Pred. No. 4.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 20

Db 516 GCAAGTGTCTAGTGGCGGG 535

RESULT 32

US-10-450-763-29555/c

; Sequence 29555, Application US/10450763

; Publication No. US20050196754A1

```

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29555
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(429)
; OTHER INFORMATION: 98% homologous to Escherichia coli rhsA,accession number
; OTHER INFORMATION: X78541,Smith-Waterman Score=744.
US-10-450-763-29555

```

```

Query Match      80.0%; Score 16.8; DB 9; Length 954;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 GCAAGTCTGTAGTGGGG 20
      ||| ||||| ||||| |||||
DB      210 GTAACGTCTGTAGTGGGG 191

```

RESULT 33

```

US-10-450-763-17672/c
; Sequence 17672, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17672
; LENGTH: 1840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1700)..(1810)
; OTHER INFORMATION: 29% homologous to Escherichia coli core protein,accession
; OTHER INFORMATION: number AF044502,Smith-Waterman Score=41.
US-10-450-763-17672

```

```

Query Match      80.0%; Score 16.8; DB 9; Length 1840;
Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 GCAAGTCTGTAGTGGGG 20
      ||| ||||| ||||| |||||
DB      210 GTAACGTCTGTAGTGGGG 191

```

RESULT 34

```

US-10-450-763-17668/c
; Sequence 17668, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17668
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(744)
; OTHER INFORMATION: 92% homologous to Escherichia coli CG Site No. 231; alternate
; OTHER INFORMATION: gene name alt,accession number U28379,Smith-Waterman Score=1162.
US-10-450-763-17668

```

```

Query Match      80.0%; Score 16.8; DB 9; Length 2178;
Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 GCAAGTCTGTAGTGGGG 20
      ||| ||||| ||||| |||||
DB      1623 GTAACGTCTGTAGTGGGG 1604

```

RESULT 35

```

US-10-450-763-25501/c
; Sequence 25501, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 25501
; LENGTH: 2179
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(744)
; OTHER INFORMATION: 92% homologous to Escherichia coli CG Site No. 231; alternate
; OTHER INFORMATION: gene name alt,accession number U28379,Smith-Waterman Score=1162.
US-10-450-763-25501

```

```

Query Match      80.0%; Score 16.8; DB 9; Length 2179;
Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 GCAAGTCTGTAGTGGGG 20
      ||| ||||| ||||| |||||
DB      1623 GTAACGTCTGTAGTGGGG 1604

```

RESULT 36
US-10-450-763-29558/c
; Sequence 29558, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29558
; LENGTH: 2250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1207)..(2208)
; OTHER INFORMATION: 98% homologous to Escherichia coli Mlc protein, accession number D90801, Smith-Waterman Score=1653.
US-10-450-763-29558

Query Match 80.0%; Score 16.8; DB 9; Length 2250;
Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
DB 663 GTAACGTCTGTAGGTGCGGG 644

RESULT 37
US-10-450-763-29562/c
; Sequence 29562, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29562
; LENGTH: 2830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1723)..(2307)
; OTHER INFORMATION: 99% homologous to Escherichia coli RhsC protein precursor, accession number D90709, Smith-Waterman Score=1050.
US-10-450-763-29562

Query Match 80.0%; Score 16.8; DB 9; Length 2830;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
DB 1965 GTAACGTCTGTAGGTGCGGG 1946

RESULT 38
US-10-450-763-25465/c
; Sequence 25465, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 25465
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (2587)..(2988)
; OTHER INFORMATION: 99% homologous to Escherichia coli rhsA, accession number X78541, Smith-Waterman Score=707.
US-10-450-763-25465

Query Match 80.0%; Score 16.8; DB 9; Length 3039;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
DB 2829 GTAACGTCTGTAGGTGCGGG 2810

RESULT 39
US-10-450-763-29044
; Sequence 29044, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29044
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (453)..(52)
; OTHER INFORMATION: 99% homologous to Escherichia coli rhsA, accession number X78541, Smith-Waterman Score=707.
US-10-450-763-29044

Query Match 80.0%; Score 16.8; DB 9; Length 3039;

; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4134)
US-10-287-274-296

Query Match 80.0%; Score 16.8; DB 6; Length 4134;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGTAGGTGCGGG 20
||| ||||| ||||| |||||
Db 243 GTAACGTCTGTAGGTGCGGG 224

RESULT 44

US-10-282-122A-6547/c
; Sequence 6547, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6547
; LENGTH: 4134
; TYPE: DNA

; ORGANISM: Escherichia coli
US-10-282-122A-6547

Query Match 80.0%; Score 16.8; DB 7; Length 4134;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGTAGGTGCGGG 20
||| ||||| ||||| |||||
Db 243 GTAACGTCTGTAGGTGCGGG 224

RESULT 45

US-10-282-122A-6875/c
; Sequence 6875, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6875
; LENGTH: 4194
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-6875

Query Match 80.0%; Score 16.8; DB 7; Length 4194;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGTAGGTGCGGG 20
||| ||||| ||||| |||||
Db 243 GTAACGTCTGTAGGTGCGGG 224

RESULT 46

US-10-282-122A-6876/c

```
; Sequence 6876, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6876
; LENGTH: 4236
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-6876

Query Match      80.0%; Score 16.8; DB 7; Length 4236;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGCGGG 20
Db 243 GTAACGTCTGTAGTGCGGG 224

RESULT 47
US-10-450-763-26014/c
; Sequence 26014, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
```

```
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 26014
; LENGTH: 5471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1864)..(926)
; OTHER INFORMATION: 96% homologous to Escherichia coli K12 putative inner
; OTHER INFORMATION: membrane component for iron transport, accession number
; OTHER INFORMATION: AE000162, Smith-Waterman Score=1505.
US-10-450-763-26014

Query Match      80.0%; Score 16.8; DB 9; Length 5471;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGCGGG 20
Db 4049 GTAACGTCTGTAGTGCGGG 4030

RESULT 48
US-10-114-170-226/c
; Sequence 226, Application US/10114170
; Publication No. US20030023075A1
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. US20030023075A1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5519
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-10-114-170-226
```

Query Match 80.0%; Score 16.8; DB 5; Length 5519;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTAGTGC GGG 20
Db 347 GTAACGTCTAGTGC GGG 328

RESULT 49

US-08-781-986A-45
; Sequence 45, Application US/08781986A
; Publication No. US20030054436A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 9072 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-781-986A-45

Query Match 80.0%; Score 16.8; DB 2; Length 9072;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTAGTGC GGG 20
Db 2901 GCAAGTTATGTAGTGC GGG 2920

RESULT 50

US-10-329-624-45
; Sequence 45, Application US/10329624
; Publication No. US20040043037A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 9072 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-329-624-45

Query Match 80.0%; Score 16.8; DB 7; Length 9072;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTAGTGC GGG 20
Db 2901 GCAAGTTATGTAGTGC GGG 2920

Search completed: January 27, 2006, 07:20:39
Job time : 350.5 secs

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:44:44 ; Search time 396 Seconds
(without alignments)
44.051 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21

Sequence: 1 cccgtgtgaggaactwtgtct 21

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA_New.*

1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.6	98.1	7979	7 US-10-509-921-9	Sequence 9, Appli
2	20.6	98.1	7979	7 US-10-509-921-10	Sequence 10, Appl
3	20.6	98.1	7979	7 US-10-509-921-11	Sequence 11, Appl
4	20.6	98.1	7979	7 US-10-509-921-12	Sequence 12, Appl
5	20.6	98.1	7980	7 US-10-509-921-4	Sequence 4, Appli
6	20.6	98.1	7980	7 US-10-509-921-5	Sequence 5, Appli
7	20.6	98.1	7983	7 US-10-509-921-7	Sequence 7, Appli
8	20.6	98.1	7989	7 US-10-509-921-2	Sequence 2, Appli
9	20.6	98.1	7989	7 US-10-509-921-6	Sequence 6, Appli
10	20.6	98.1	7989	7 US-10-509-921-8	Sequence 8, Appli
11	20.6	98.1	7989	7 US-10-509-921-13	Sequence 13, Appl
12	20.6	98.1	7989	7 US-10-509-921-14	Sequence 14, Appl
13	20.6	98.1	7992	8 US-11-119-330-1	Sequence 1, Appli
14	20.6	98.1	7992	8 US-10-509-921-3	Sequence 3, Appli
15	20.6	98.1	7992	8 US-11-111-686-1	Sequence 1, Appli
16	20.6	98.1	7992	8 US-11-111-686-2	Sequence 2, Appli
17	20.6	98.1	7992	8 US-11-111-686-4	Sequence 4, Appli
18	20.6	98.1	7992	8 US-11-111-686-5	Sequence 5, Appli
19	20.6	98.1	7992	8 US-11-111-686-6	Sequence 6, Appli
20	20.6	98.1	7995	8 US-11-111-686-3	Sequence 3, Appli
21	20.6	98.1	9599	7 US-10-985-205-1	Sequence 1, Appli
22	17	81.0	1094	7 US-10-750-185-51689	Sequence 51689, A

c	23	17	81.0	1094	7	US-10-750-623-51689	Sequence 51689, A
	24	17	81.0	3216	7	US-10-750-185-39720	Sequence 39720, A
	25	17	81.0	3216	7	US-10-750-623-39720	Sequence 39720, A
	26	16.4	78.1	1752	7	US-10-750-185-37350	Sequence 37350, A
	27	16.4	78.1	1752	7	US-10-750-623-37350	Sequence 37350, A
	28	15.8	75.2	509	8	US-11-020-772-32	Sequence 32, Appli
c	29	15.8	75.2	877	7	US-10-750-185-36885	Sequence 36885, A
c	30	15.8	75.2	877	7	US-10-750-623-36885	Sequence 36885, A
c	31	15.8	75.2	2226	7	US-10-750-185-24847	Sequence 24847, A
c	32	15.8	75.2	2226	7	US-10-750-623-24847	Sequence 24847, A
c	33	15.8	75.2	3338	7	US-10-750-185-26147	Sequence 26147, A
c	34	15.8	75.2	3338	7	US-10-750-623-26147	Sequence 26147, A
c	35	15.8	75.2	3534	7	US-10-750-185-36810	Sequence 36810, A
c	36	15.8	75.2	3534	7	US-10-750-623-36810	Sequence 36810, A
c	37	15.8	75.2	147700	7	US-10-857-780-3	Sequence 3, Appli
c	38	15.8	75.2	149419	8	US-11-112-908-49	Sequence 49, Appli
c	39	15.8	75.2	166111	8	US-11-112-908-47	Sequence 47, Appli
c	40	15.4	73.3	600	7	US-10-750-185-460	Sequence 460, App
c	41	15.4	73.3	600	7	US-10-750-623-460	Sequence 460, App
c	42	15.4	73.3	670	7	US-10-750-185-61723	Sequence 61723, A
c	43	15.4	73.3	670	7	US-10-750-623-61723	Sequence 61723, A
c	44	15.4	73.3	1374	7	US-10-750-185-51706	Sequence 51706, A
c	45	15.4	73.3	1374	7	US-10-750-623-51706	Sequence 51706, A
c	46	15.4	73.3	1467	7	US-10-750-185-38999	Sequence 38999, A
c	47	15.4	73.3	1467	7	US-10-750-623-38999	Sequence 38999, A
c	48	15.4	73.3	1493	8	US-11-136-527-2274	Sequence 2274, Ap
c	49	15.4	73.3	3443	8	US-11-136-527-3734	Sequence 3734, Ap
c	50	15.4	73.3	5506	7	US-10-821-234-277	Sequence 277, Appli
c	51	15.4	73.3	5510	8	US-11-150-406-1	Sequence 1, Appli
c	52	15.2	72.4	25	8	US-11-121-849-409578	Sequence 409578, A
c	53	15.2	72.4	201	7	US-10-995-561-28272	Sequence 28272, A
c	54	15.2	72.4	201	7	US-10-995-561-61097	Sequence 61097, A
c	55	15.2	72.4	786	7	US-10-750-185-32024	Sequence 32024, A
c	56	15.2	72.4	786	7	US-10-750-623-32024	Sequence 32024, A
c	57	15.2	72.4	813	7	US-10-750-185-53254	Sequence 53254, A
c	58	15.2	72.4	813	7	US-10-750-623-53254	Sequence 53254, A
c	59	15.2	72.4	88116	7	US-10-995-561-13351	Sequence 13351, A
c	60	15.2	72.4	222094	7	US-10-995-561-13244	Sequence 13244, A
c	61	15.2	72.4	222094	7	US-11-121-849-311219	Sequence 311219, A
c	62	15.2	71.4	876	7	US-10-750-185-48349	Sequence 48349, A
c	63	15.2	71.4	876	7	US-10-750-623-48349	Sequence 48349, A
c	64	15.2	71.4	1432	7	US-10-750-185-51771	Sequence 51771, A
c	65	15.2	71.4	1432	7	US-10-750-623-51771	Sequence 51771, A
c	66	15.2	71.4	1783	7	US-10-750-185-48464	Sequence 48464, A
c	67	15.2	71.4	1783	7	US-10-750-623-48464	Sequence 48464, A
c	68	15.2	71.4	189539	8	US-11-121-086-15	Sequence 16, Appli
c	69	14.8	70.5	19	9	US-11-101-244-1059418	Sequence 1059418, A
c	70	14.8	70.5	19	10	US-11-083-784-1059418	Sequence 1059418, A
c	71	14.8	70.5	25	8	US-11-121-849-536730	Sequence 536730, A
c	72	14.8	70.5	25	8	US-10-310-914A-18319	Sequence 18319, A
c	73	14.8	70.5	201	7	US-10-995-561-31062	Sequence 31062, A
c	74	14.8	70.5	201	8	US-11-124-368A-20547	Sequence 20547, A
c	75	14.8	70.5	201	8	US-11-124-368A-20939	Sequence 20939, A
c	76	14.8	70.5	201	8	US-11-124-368A-21039	Sequence 21039, A
c	77	14.8	70.5	575	8	US-11-000-688-1285	Sequence 1285, Ap
c	78	14.8	70.5	720	8	US-11-118-855-3	Sequence 3, Appli
c	79	14.8	70.5	1947	7	US-10-750-185-49960	Sequence 49960, A
c	80	14.8	70.5	1947	7	US-10-750-623-49960	Sequence 49960, A
c	81	14.8	70.5	2251	7	US-10-750-185-60956	Sequence 60956, A
c	82	14.8	70.5	2251	7	US-10-750-623-60956	Sequence 60956, A
c	83	14.8	70.5	2454	8	US-11-000-688-1287	Sequence 1287, Ap
c	84	14.8	70.5	2462	8	US-11-136-527-364	Sequence 264, App
c	85	14.8	70.5	2879	8	US-11-124-368A-166	Sequence 166, App
c	86	14.8	70.5	3260	8	US-11-136-527-2356	Sequence 2356, Ap
c	87	14.8	70.5	3583	8	US-11-136-527-615	Sequence 615, App
c	88	14.8	70.5	15660	8	US-10-453-372-1001	Sequence 1001, Ap
c	89	14.8	70.5	18755	8	US-11-124-368A-2931	Sequence 2931, Ap
c	90	14.8	70.5	41081	8	US-11-124-368A-2931	Sequence 2931, Ap
c	91	14.8	70.5	65723	7	US-10-995-561-13200	Sequence 13200, A
c	92	14.8	70.5	100387	8	US-11-121-086-94	Sequence 94, Appli
c	93	14.8	70.5	103660	7	US-10-995-561-13253	Sequence 13253, A
c	94	14.8	70.5	136284	7	US-10-775-169-149	Sequence 149, App
c	95	14.8	70.5	212716	8	US-11-121-086-95	Sequence 95, Appli

Sequence 1, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 181, App
Sequence 183, App

ALIGNMENTS

RESULT 1

US-10-509-921-9
; Sequence 9, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 7979
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV J4(B/R1) Replicons
US-10-509-921-9

Query Match 98.1%; Score 20.6; DB 7; Length 7979;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 2

US-10-509-921-10
; Sequence 10, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 7979
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV J4(J4B/R1(C))Replicons
US-10-509-921-10

Query Match 98.1%; Score 20.6; DB 7; Length 7979;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 3

US-10-509-921-11
; Sequence 11, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7979
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV J4 Replicons
US-10-509-921-11

Query Match 98.1%; Score 20.6; DB 7; Length 7979;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 4

US-10-509-921-12
; Sequence 12, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 7979
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV J4 Replicons
US-10-509-921-12

Query Match 98.1%; Score 20.6; DB 7; Length 7979;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 5

US-10-509-921-4
; Sequence 4, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335

; CURRENT APPLICATION NUMBER: US/10/509,921
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7980
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV H77(BB7-F3)Replicons
US-10-509-921-4

Query Match 98.1%; Score 20.6; DB 7; Length 7980;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 6

US-10-509-921-5
; Sequence 5, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7980
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV H77 (BB7-F3(C)) Replicons
US-10-509-921-5

Query Match 98.1%; Score 20.6; DB 7; Length 7980;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 7

US-10-509-921-7
; Sequence 7, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7983
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV 1a Replicons
US-10-509-921-7

Query Match 98.1%; Score 20.6; DB 7; Length 7983;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 8

US-10-509-921-2
; Sequence 2, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV H77 (BB7-F1)Replicons
US-10-509-921-2

Query Match 98.1%; Score 20.6; DB 7; Length 7989;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 9

US-10-509-921-6
; Sequence 6, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV H77(BB7/H77NSSB)Replicons
US-10-509-921-6

Query Match 98.1%; Score 20.6; DB 7; Length 7989;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 10

US-10-509-921-8
 ; Sequence 8, Application US/10509921
 ; Publication No. US20050250093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SmithKline Beecham Corporation
 ; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
 ; FILE REFERENCE: P51335
 ; CURRENT APPLICATION NUMBER: US/10/509,921
 ; CURRENT FILING DATE: 2004-10-01
 ; PRIOR APPLICATION NUMBER: 60/369,685
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; TYPE: DNA
 ; LENGTH: 7989
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
 ; OTHER INFORMATION: HCV J4(J4 M/S)Replicons
 US-10-509-921-8

Query Match 98.1%; Score 20.6; DB 7; Length 7989;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 11

US-10-509-921-13
 ; Sequence 13, Application US/10509921
 ; Publication No. US20050250093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SmithKline Beecham Corporation
 ; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
 ; FILE REFERENCE: P51335
 ; CURRENT APPLICATION NUMBER: US/10/509,921
 ; CURRENT FILING DATE: 2004-10-01
 ; PRIOR APPLICATION NUMBER: 60/369,685
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; TYPE: DNA
 ; LENGTH: 7989
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
 ; OTHER INFORMATION: HCV J4(BB7/J4NS5B)Replicons
 US-10-509-921-13

Query Match 98.1%; Score 20.6; DB 7; Length 7989;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 12

US-10-509-921-14
 ; Sequence 14, Application US/10509921

; Publication No. US20050250093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SmithKline Beecham Corporation
 ; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
 ; FILE REFERENCE: P51335
 ; CURRENT APPLICATION NUMBER: US/10/509,921
 ; CURRENT FILING DATE: 2004-10-01
 ; PRIOR APPLICATION NUMBER: 60/369,685
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 7989
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
 ; OTHER INFORMATION: HCV H77(pBB7-SN)Replicons
 US-10-509-921-14

Query Match 98.1%; Score 20.6; DB 7; Length 7989;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 13

US-11-119-330-1
 ; Sequence 1, Application US/11119330
 ; Publication No. US20050260568A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Min
 ; APPLICANT: Lemm, Julie A.
 ; APPLICANT: O'Boyle, Donald R.
 ; APPLICANT: Nowar, Peter
 ; TITLE OF INVENTION: HEPATITIS C VIRUS ASSAYS
 ; FILE REFERENCE: 10283 NP
 ; CURRENT APPLICATION NUMBER: US/11/119,330
 ; CURRENT FILING DATE: 2005-04-29
 ; PRIOR APPLICATION NUMBER: 60/567,270
 ; PRIOR FILING DATE: 2004-04-30
 ; PRIOR APPLICATION NUMBER: 60/568,590
 ; PRIOR FILING DATE: 2004-05-06
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1
 ; LENGTH: 7989
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HCV Replicon
 US-11-119-330-1

Query Match 98.1%; Score 20.6; DB 8; Length 7989;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 14

US-10-509-921-3
 ; Sequence 3, Application US/10509921
 ; Publication No. US20050250093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SmithKline Beecham Corporation
 ; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
 ; FILE REFERENCE: P51335

; CURRENT APPLICATION NUMBER: US/10/509,921
 ; CURRENT FILING DATE: 2004-10-01
 ; PRIOR APPLICATION NUMBER: 60/369,685
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3:
 ; LENGTH: 7992
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
 ; OTHER INFORMATION: HCV H77(BB7-Fl/P2) Replicons
 US-10-509-921-3

Query Match 98.1%; Score 20.6; DB 7; Length 7992;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACACTWCTGTCT 21
 Db 43 CCCTGTGAGGAACACTGTCT 63

RESULT 15

US-11-111-686-1
 ; Sequence 1, Application US/11111686
 ; Publication No. US20050260221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANADYS Pharmaceuticals, Inc.
 ; APPLICANT: Bichko, Vadim
 ; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REP
 ; FILE REFERENCE: 0342/1H395US1
 ; CURRENT APPLICATION NUMBER: US/11/111,686
 ; CURRENT FILING DATE: 2005-04-20
 ; PRIOR APPLICATION NUMBER: US/10/005,469
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/245,866
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 7992
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HCV replicon I377/NS3-3'UTR
 US-11-111-686-1

Query Match 98.1%; Score 20.6; DB 8; Length 7992;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACACTWCTGTCT 21
 Db 43 CCCTGTGAGGAACACTGTCT 63

RESULT 16

US-11-111-686-2
 ; Sequence 2, Application US/11111686
 ; Publication No. US20050260221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANADYS Pharmaceuticals, Inc.
 ; APPLICANT: Bichko, Vadim
 ; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REP
 ; FILE REFERENCE: 0342/1H395US1
 ; CURRENT APPLICATION NUMBER: US/11/111,686
 ; CURRENT FILING DATE: 2005-04-20
 ; PRIOR APPLICATION NUMBER: US/10/005,469
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/245,866
 ; PRIOR FILING DATE: 2000-11-07

; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 7992
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR2
 US-11-111-686-2

Query Match 98.1%; Score 20.6; DB 8; Length 7992;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACACTWCTGTCT 21
 Db 43 CCCTGTGAGGAACACTGTCT 63

RESULT 17

US-11-111-686-4
 ; Sequence 4, Application US/11111686
 ; Publication No. US20050260221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANADYS Pharmaceuticals, Inc.
 ; APPLICANT: Bichko, Vadim
 ; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
 ; FILE REFERENCE: 0342/1H395US1
 ; CURRENT APPLICATION NUMBER: US/11/111,686
 ; CURRENT FILING DATE: 2005-04-20
 ; PRIOR APPLICATION NUMBER: US/10/005,469
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/245,866
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 7992
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR9
 US-11-111-686-4

Query Match 98.1%; Score 20.6; DB 8; Length 7992;
 Best Local Similarity 95.2%; Pred. No. 0.44;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACACTWCTGTCT 21
 Db 43 CCCTGTGAGGAACACTGTCT 63

RESULT 18

US-11-111-686-5
 ; Sequence 5, Application US/11111686
 ; Publication No. US20050260221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANADYS Pharmaceuticals, Inc.
 ; APPLICANT: Bichko, Vadim
 ; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
 ; FILE REFERENCE: 0342/1H395US1
 ; CURRENT APPLICATION NUMBER: US/11/111,686
 ; CURRENT FILING DATE: 2005-04-20
 ; PRIOR APPLICATION NUMBER: US/10/005,469
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/245,866
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 7992
 ; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon from cell line HCVR22
US-11-111-686-5

Query Match      98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21
   |||||
Db 43 CCTGTGAGGAAGTCTGCT 63
   |||||

RESULT 19
US-11-111-686-6
; Sequence 6, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon from cell line HCVR24
US-11-111-686-6

Query Match      98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21
   |||||
Db 43 CCTGTGAGGAAGTCTGCT 63
   |||||

RESULT 20
US-11-111-686-3
; Sequence 3, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 7995
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR8
US-11-111-686-3
```

```
Query Match      98.1%; Score 20.6; DB 8; Length 7995;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21
   |||||
Db 43 CCTGTGAGGAAGTCTGCT 63
   |||||

RESULT 21
US-10-985-205-1
; Sequence 1, Application US/10985205
; Publication No. US20050266400A1
; GENERAL INFORMATION:
; APPLICANT: Dumonceaux, Julie
; APPLICANT: Cormier, Emmanuel G.
; APPLICANT: Gardner, Jason P.
; APPLICANT: Dragic, Tatjana
; TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS
; FILE REFERENCE: 71242-A/JPW/AJD
; CURRENT APPLICATION NUMBER: US/10/985,205
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/519,536
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9599
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-985-205-1

Query Match      98.1%; Score 20.6; DB 7; Length 9599;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21
   |||||
Db 43 CCTGTGAGGAAGTCTGCT 63
   |||||

RESULT 22
US-10-750-185-51689/c
; Sequence 51689, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MW1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51689
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine 19866880406659
US-10-750-185-51689

Query Match      81.0%; Score 17; DB 7; Length 1094;
Best Local Similarity 89.5%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 19
   |||||
```

Db 144 CCTGTGAGGAACCTTCTAT 126

RESULT 23

US-10-750-623-51689/c
; Sequence 51689, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51689
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine 19866880406659
US-10-750-623-51689

Query Match 81.0%; Score 17; DB 7; Length 1094;
Best Local Similarity 89.5%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 19
|||||
Db 144 CCTGTGAGGAACCTTCTAT 126

RESULT 24

US-10-750-185-39720
; Sequence 39720, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39720
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Bovine 19866881421275
US-10-750-185-39720

Query Match 81.0%; Score 17; DB 7; Length 3216;
Best Local Similarity 89.5%; Pred. No. 27;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 19
|||||
Db 2155 CCTTTGAGGAACCTTCTGT 2173

RESULT 25

US-10-750-623-39720
; Sequence 39720, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39720
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Bovine 19866881421275
US-10-750-623-39720

Query Match 81.0%; Score 17; DB 7; Length 3216;
Best Local Similarity 89.5%; Pred. No. 27;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 19
|||||
Db 2155 CCTTTGAGGAACCTTCTGT 2173

RESULT 26

US-10-750-185-37350
; Sequence 37350, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37350
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Bovine 19866880501591
US-10-750-185-37350

Query Match 78.1%; Score 16.4; DB 7; Length 1752;
Best Local Similarity 85.0%; Pred. No. 51;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 20
|||||
Db 665 CCTTTGAGGAACCTTCTGT 684

RESULT 27

US-10-750-623-37350
; Sequence 37350, Application US/10750623

```
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37350
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Bovine 19866880501591
US-10-750-623-37350

Query Match      78.1%; Score 16.4; DB 7; Length 1752;
Best Local Similarity 85.0%; Pred. No. 51;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 20
Db 665 CCTTGTGAGGAGCTTCTGTC 684

RESULT 28
US-11-020-772-32
; Sequence 32, Application US/11020772
; Publication No. US20050256043A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig, Linda B.
; TITLE OF INVENTION: HIV Antisense Proteins
; FILE REFERENCE: 25125,0001
; CURRENT APPLICATION NUMBER: US/11/020,772
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 09/249,542
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,640
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 08/853,703
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 32
; LENGTH: 509
; TYPE: RNA
; ORGANISM: human immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: HIV antisense HAP gene (clade A)
US-11-020-772-32

Query Match      75.2%; Score 15.8; DB 8; Length 509;
Best Local Similarity 52.4%; Pred. No. 86;
Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 128 CCCUGUCAGCAUCUGUGU 148

RESULT 29
US-10-750-185-36885/c
; Sequence 36885, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
```

```
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36885
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866880749700
US-10-750-185-36885

Query Match      75.2%; Score 15.8; DB 7; Length 877;
Best Local Similarity 81.0%; Pred. No. 93;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 37 CCCTGTGAGGACCCACTGGCT 17

RESULT 30
US-10-750-623-36885/c
; Sequence 36885, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36885
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866880749700
US-10-750-623-36885

Query Match      75.2%; Score 15.8; DB 7; Length 877;
Best Local Similarity 81.0%; Pred. No. 93;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 37 CCCTGTGAGGACCCACTGGCT 17

RESULT 31
US-10-750-185-24847
; Sequence 24847, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
```

APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 24847
LENGTH: 2226
TYPE: DNA
ORGANISM: Bovine 19866880668698
US-10-750-185-24847

Query Match 75.2%; Score 15.8; DB 7; Length 2226;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGT 19
|||||
Db 937 CCCTGTGAGGAAGTCTGT 955

RESULT 32
US-10-750-623-24847
Sequence 24847, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 24847
LENGTH: 2226
TYPE: DNA
ORGANISM: Bovine 19866880668698
US-10-750-623-24847

Query Match 75.2%; Score 15.8; DB 7; Length 2226;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGT 19
|||||
Db 937 CCCTGTGAGGAAGTCTGT 955

RESULT 33
US-10-750-185-26147/c
Sequence 26147, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 26147
LENGTH: 3338
TYPE: DNA
ORGANISM: Bovine 19866881385217
US-10-750-185-26147

Query Match 75.2%; Score 15.8; DB 7; Length 3338;
Best Local Similarity 81.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 911 CCAGTGGGGAAGTCTGTCT 891

RESULT 34
US-10-750-623-26147/c
Sequence 26147, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 26147
LENGTH: 3338
TYPE: DNA
ORGANISM: Bovine 19866881385217
US-10-750-623-26147

Query Match 75.2%; Score 15.8; DB 7; Length 3338;
Best Local Similarity 81.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 911 CCAGTGGGGAAGTCTGTCT 891

RESULT 35
US-10-750-185-36810/c
Sequence 36810, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31

```
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36810
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Bovine 19866880404939
US-10-750-185-36810

Query Match          75.2%; Score 15.8; DB 7; Length 3534;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
    |||||
Db 1802 CTCTGTGAGGAAGTCTGTCT 1782

RESULT 36
US-10-750-623-36810/c
; Sequence 36810, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36810
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Bovine 19866880404939
US-10-750-623-36810

Query Match          75.2%; Score 15.8; DB 7; Length 3534;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
    |||||
Db 1802 CTCTGTGAGGAAGTCTGTCT 1782

RESULT 37
US-10-857-780-3
; Sequence 3, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
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; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 147700
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51510)..(51510)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51526)..(51526)
; OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-3

Query Match          75.2%; Score 15.8; DB 7; Length 147700;
Best Local Similarity 81.0%; Pred. No. 2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
    |||||
Db 121582 CCTGTGAGGAAGTCTGTCT 121602

RESULT 38
US-11-112-908-49/c
; Sequence 49, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 149419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-49

Query Match          75.2%; Score 15.8; DB 8; Length 149419;
Best Local Similarity 81.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
    |||||
Db 117999 CCTGTGAGGAAGTCTGTCT 117979

RESULT 39
US-11-112-908-47/c
; Sequence 47, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
```

; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 166111
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-47

Query Match 75.2%; Score 15.8; DB 8; Length 166111;
Best Local Similarity 81.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21
Db 95099 CCTGTGAGGAACTWCTGTCT 95079

RESULT 40
US-10-750-185-460
; Sequence 460, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 460
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT08269
US-10-750-185-460

Query Match 73.3%; Score 15.4; DB 7; Length 600;
Best Local Similarity 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 19
Db 20 CCTGTGAGGAACTWCTGTCT 38

RESULT 41
US-10-750-623-460
; Sequence 460, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 460
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT08269
US-10-750-623-460

Query Match 73.3%; Score 15.4; DB 7; Length 600;
Best Local Similarity 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 19
Db 20 CCTGTGAGGAACTWCTGTCT 38

RESULT 42
US-10-750-185-61723
; Sequence 61723, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61723
; LENGTH: 670
; TYPE: DNA
; ORGANISM: Bovine 19866880649350
US-10-750-185-61723

Query Match 73.3%; Score 15.4; DB 7; Length 670;
Best Local Similarity 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CTGTGAGGAACTWCTGTCT 21
Db 508 CTGTGAGGAACTWCTGTCT 526

RESULT 43
US-10-750-623-61723
; Sequence 61723, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1

```
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61723
; TYPE: DNA
; ORGANISM: Bovine 19866880649350
US-10-750-623-61723

Query Match      73.3%; Score 15.4; DB 7; Length 670;
Best Local Similarity 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 CTGTGAGGAAGTCTCTCT 21
DB      508 CTGTGAGGAAGTCTCTCT 526

RESULT 44
US-10-750-185-51706
; Sequence 51706, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51706
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Bovine 19866881516841
US-10-750-185-51706

Query Match      73.3%; Score 15.4; DB 7; Length 1374;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 CTGTGAGGAAGTCTCTCT 21
DB      737 CTGTGAGGAAGTCTCTCT 755

RESULT 45
US-10-750-623-51706
; Sequence 51706, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51706
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Bovine 19866881516841
US-10-750-623-51706

Query Match      73.3%; Score 15.4; DB 7; Length 1374;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 CTGTGAGGAAGTCTCTCT 21
DB      737 CTGTGAGGAAGTCTCTCT 755

RESULT 46
US-10-750-185-38999
; Sequence 38999, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 38999
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Bovine 19866880809379
US-10-750-185-38999

Query Match      73.3%; Score 15.4; DB 7; Length 1467;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAAGTCTCTGT 19
DB      682 CCCTGTGAGGAAGTCTCTGT 700

RESULT 47
US-10-750-623-38999
; Sequence 38999, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 38999
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Bovine 19866880809379
US-10-750-623-38999

Query Match      73.3%; Score 15.4; DB 7; Length 1467;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAAGTCTCTGT 19
DB      682 CCCTGTGAGGAAGTCTCTGT 700
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```
; SEQ ID NO 38999
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Bovine 19866880809379
US-10-750-623-38999

Query Match          73.3%; Score 15.4; DB 7; Length 1467;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACCTWCTGT 19
        ||||| ||||| ||||| |||||
Db       682 CCCTGTGGTAACTTCTGT 700

RESULT 48
US-11-136-527-2274/c
; Sequence 2274, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2274
; LENGTH: 1493
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2274

Query Match          73.3%; Score 15.4; DB 8; Length 1493;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 CCTGTGAGGAACCTWCTGTC 20
        ||||| ||||| ||||| |||||
Db       782 CCTGTGAGGAATACTGTC 764

RESULT 49
US-11-136-527-3734/c
; Sequence 3734, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3734
; LENGTH: 3443
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3734

Query Match          73.3%; Score 15.4; DB 8; Length 3443;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 CCTGTGAGGAACCTWCTGTC 20
        ||||| ||||| ||||| |||||
Db       1862 CCTGTGAGGAATACTGTC 1844
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RESULT 50
US-10-821-234-277
; Sequence 277, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 277
; LENGTH: 5506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-277

Query Match          73.3%; Score 15.4; DB 7; Length 5506;
Best Local Similarity 84.2%; Pred. No. 2e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACCTWCTGT 19
        ||||| ||||| ||||| |||||
Db       2895 CCCTGTGAGGCACCTTCTGT 2913
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Search completed: January 27, 2006, 07:33:55
Job time : 397 secs

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:37:30 ; Search time 348.5 Seconds
(without alignments)
498.298 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21
Sequence: 1 ccctgtgaggaactwctgtct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	100%

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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

```

[illegible]


```
US-09-782-361-1
; Sequence 1, Application US/09782361
; Patent No. US20020064778A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sense universal primer for PCR (first round)
US-09-782-361-1

Query Match          98.1%; Score 20.6; DB 3; Length 25;
Best Local Similarity 95.2%; Pred. No. 0.81;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
Db 4 CCCTGTGAGGAAGTCTGTCT 24

RESULT 6
US-09-294-121A-1
; Sequence 1, Application US/09294121A
; Patent No. US20020069422A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,121A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002

US-09-782-361-1
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr98"
US-09-294-121A-1

Query Match          98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 7
US-09-899-082A-1
; Sequence 1, Application US/09899082A
; Patent No. US2002010638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
```

TELEFAX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: HCV
 MAP POSITION: Position -299 of 5' end
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..27
 OTHER INFORMATION: /standard_name="Universal HCV primer HcPr98"
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-899-082A-1
 Query Match 98.1%; Score 20.6; DB 3; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 Db 1 CCCTGTGAGGAAGTCTGTCT 21
 |||||
 RESULT 8
 US-09-899-302-1
 ; Sequence 1, Application US/09899302
 ; Patent No. US20020168626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
 ; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
 ; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
 ; TITLE OF INVENTION: ISOLATES
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIERMAN & MUSERLIAN
 ; STREET: 600 THIRD AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10016
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/899,302
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/378,900
 ; FILING DATE:
 ; APPLICATION NUMBER: 08/256,568
 ; FILING DATE: 18-JUL-1994
 ; APPLICATION NUMBER: PCT/EP93/03325
 ; FILING DATE: 26-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP/93/402,129.6
 ; FILING DATE: 31-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP/92/403,222.0
 ; FILING DATE: 27-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CHARLES A. MUSERLIAN
 ; REGISTRATION NUMBER: 19,683

```
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard_name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-899-044-1
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Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21
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RESULT 10
US-10-407-897-78
; Sequence 78, Application US/10407897
; Publication No. US20040072148A1
; GENERAL INFORMATION:
; APPLICANT: Ji, Jiuping
; APPLICANT: Manak, Mark
; APPLICANT: Gonzalez, Irene
; TITLE OF INVENTION: Simultaneous Detection of HBV, HCV, and HIV in Plasma Samples
; TITLE OF INVENTION: Using a Multiplex Capture Assay
; FILE REFERENCE: 1589.0280002
; CURRENT APPLICATION NUMBER: US/10/407,897
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 10/130,533
; PRIOR FILING DATE: 2002-11-17
; PRIOR APPLICATION NUMBER: PCT/US00/31738
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/165,916
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Primer
US-10-407-897-78
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Query Match 98.1%; Score 20.6; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21
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RESULT 11
US-10-822-711-1
; Sequence 1, Application US/10822711
; Publication No. US20040191768A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/822,711
; FILING DATE: 13-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-Jul-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 28-Nov-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-Aug-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-Nov-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEtical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard_name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-822-711-1
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Query Match 98.1%; Score 20.6; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCTGTGAGGAAGTCTGTCT 21
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Fri Jan 27 09:12:35 2006

us-10-070-415a-1.rnpbm

Db 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

RESULT 12
US-10-363-177A-5
; Sequence 5, Application US/10363177A
; Publication No. US20050084851A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
; APPLICANT: Ronaghi, Mostafa
; APPLICANT: Pourmand, Nader
; APPLICANT: Ekstrom, Bjorn
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
; FILE REFERENCE: Docket 14629
; CURRENT APPLICATION NUMBER: US/10/363,177A
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Synthetic Oligonucleotide HCV-PCR-OUTF
US-10-363-177A-5

Query Match 98.1%; Score 20.6; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 13
US-10-070-415A-30
; Sequence 30, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, Koji
; APPLICANT: ASHIMOTO, Michie
; APPLICANT: MASHIRO, Shunji
; APPLICANT: OOTA, Yasuhiko
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
; FILE REFERENCE: 220633US2SRDPT
; CURRENT APPLICATION NUMBER: US/10/070,415A
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: PCT/JP02/02030
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: JP 2001-090053
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 30
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-070-415A-30

Query Match 98.1%; Score 20.6; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

Db 16 CCCTGTGAGGAAGTCTGTCT 36

RESULT 14

US-09-728-265-22/c
; Sequence 22, Application US/09729265
; Publication No. US20020182598A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
; TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroock & Stroock & Lavan
; STREET: 180 Maiden Lane
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10038
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/728,265
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokotilow, Steven B
; REGISTRATION NUMBER: 26,405
; REFERENCE/DOCKET NUMBER: Old 29545APCT/USA-B // New 251305/0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212806-6663
; TELEFAX: 2128066006
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..45
US-09-728-265-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.85;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 15

US-09-978-261A-22/c
; Sequence 22, Application US/09978261A
; Publication No. US20030175706A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHODS
; FILE REFERENCE: A29545-A-PCT-USA-A 070165.0601
; CURRENT APPLICATION NUMBER: US/09/978,261A
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; PRIOR APPLICATION NUMBER: 08/596,331
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/690,495
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: 08/909,031
; PRIOR FILING DATE: 1997-08-11

; PRIOR APPLICATION NUMBER: 09/728,265
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-978-261A-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.85;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 16

US-10-309-438-22/c
; Sequence 22, Application US/10309438
; Publication No. US20030190604A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Brandwein, Maragat
; APPLICANT: Heuh, Terence C.H.
; TITLE OF INVENTION: Nucleic Acid Amplification Method: Ramification-extension
; FILE REFERENCE: 251305/0031
; CURRENT APPLICATION NUMBER: US/10/309,438
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 09/299,217
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 08/690,494
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: US 08/596,331
; PRIOR FILING DATE: 1996-05-20
; PRIOR APPLICATION NUMBER: PCT/US95/07671
; PRIOR FILING DATE: 1995-06-14
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-309-438-22

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.85;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 17

US-10-719-480-22/c
; Sequence 22, Application US/10719480
; Publication No. US20040137484A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Yi, Jizu
; APPLICANT: Zhang, Wand
; TITLE OF INVENTION: Nucleic Acid Amplification Methods
; FILE REFERENCE: 251305/0040

; CURRENT APPLICATION NUMBER: US/10/719,480
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 09/978,261
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/US02/32754
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-719-480-22

Query Match 98.1%; Score 20.6; DB 7; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.85;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 18

US-10-451-882-41
; Sequence 41, Application US/10451882
; Publication No. US20040185455A1
; GENERAL INFORMATION:
; APPLICANT: Takara Shuzo Co., Ltd.
; TITLE OF INVENTION: Method for detection of virulent organisms
; FILE REFERENCE: 662981
; CURRENT APPLICATION NUMBER: US/10/451,882
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: JP 2000-396321
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2000-396222
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2001-199552
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: JP 2001-278920
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 41
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer area to amplify a portion of HCV.
US-10-451-882-41

Query Match 98.1%; Score 20.6; DB 8; Length 73;
Best Local Similarity 95.2%; Pred. No. 0.88;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 21 CCTGTGAGGAAGTCTGTCT 41

RESULT 19

US-10-333-449A-28
; Sequence 28, Application US/10333449A
; Publication No. US20040137424A1
; GENERAL INFORMATION:
; APPLICANT: Tan, Yin Hwee
; APPLICANT: Lim, Siew Pheng
; APPLICANT: Lim, Seng Gee
; APPLICANT: Hong, Wan Jin
; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR DETECTING VIRAL INFECTION,
; TITLE OF INVENTION: UNCOVERING ANTI-VIRAL DRUG CANDIDATES AND DETERMINING DRUG
; FILE OF INVENTION: RESISTANCE OF VIRAL ISOLATES

[illegible]

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Db 1 CCCTGTGAGGAACCTCTGTCT 21

RESULT 24
US-10-363-177A-67
; Sequence 67, Application US/10363177A
; Publication No. US20050084851A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
; APPLICANT: Ronaghi, Mostafa
; APPLICANT: Pourmand, Nader
; APPLICANT: Ekstrom, Bjorn
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
; FILE REFERENCE: Docket 14629
; CURRENT APPLICATION NUMBER: US/10/363,177A
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-363-177A-67

Query Match 98.1%; Score 20.6; DB 9; Length 278;
Best Local Similarity 95.2%; Pred. No. 0.98;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTCTGTCT 21
|||||:|||||:|||||:|||||:
Db 1 CCCTGTGAGGAACCTCTGTCT 21

RESULT 25
US-09-345-761-7
; Sequence 7, Application US/09345761
; Patent No. US20010053518A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/09/345,761
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-09-345-761-7

Query Match 98.1%; Score 20.6; DB 3; Length 298;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTCTGTCT 21
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Db 29 CCUGUGAGGAACUACUGUCU 49

RESULT 26
US-10-687-588-7
; Sequence 7, Application US/10687588
; Publication No. US20040115718A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
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; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/10/687,588
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/09/345,761
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-10-687-588-7

Query Match 98.1%; Score 20.6; DB 7; Length 298;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTCTGTCT 21
|||||:|||||:|||||:|||||:
Db 29 CCUGUGAGGAACUACUGUCU 49

RESULT 27
US-10-230-381-1
; Sequence 1, Application US/10230381
; Publication No. US20030152591A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,
; FILE REFERENCE: INNX-124-EP
; CURRENT APPLICATION NUMBER: US/10/230,381
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 299
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-10-230-381-1

Query Match 98.1%; Score 20.6; DB 6; Length 299;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTCTGTCT 21
|||||:|||||:|||||:|||||:
Db 1 CCCTGTGAGGAACCTCTGTCT 21

RESULT 28
US-10-363-177A-63
; Sequence 63, Application US/10363177A
; Publication No. US20050084851A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
; APPLICANT: Ronaghi, Mostafa
; APPLICANT: Pourmand, Nader
; APPLICANT: Ekstrom, Bjorn
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
; FILE REFERENCE: Docket 14629
; CURRENT APPLICATION NUMBER: US/10/363,177A
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Hepatitis C virus
```

US-10-363-177A-63

Query Match 98.1%; Score 20.6; DB 9; Length 305;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 29

US-10-363-177A-64
 ; Sequence 64, Application US/10363177A
 ; Publication No. US20050084851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyrosequencing AB
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
 ; APPLICANT: Ronaghi, Mostafa
 ; APPLICANT: Pourmand, Nader
 ; APPLICANT: Ekstrom, Bjorn
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
 ; FILE REFERENCE: Docket 14629
 ; CURRENT APPLICATION NUMBER: US/10/363,177A
 ; CURRENT FILING DATE: 2003-03-06
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 64
 ; LENGTH: 305
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 US-10-363-177A-64

Query Match 98.1%; Score 20.6; DB 9; Length 305;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 30

US-10-363-177A-65
 ; Sequence 65, Application US/10363177A
 ; Publication No. US20050084851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyrosequencing AB
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
 ; APPLICANT: Ronaghi, Mostafa
 ; APPLICANT: Pourmand, Nader
 ; APPLICANT: Ekstrom, Bjorn
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
 ; FILE REFERENCE: Docket 14629
 ; CURRENT APPLICATION NUMBER: US/10/363,177A
 ; CURRENT FILING DATE: 2003-03-06
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 65
 ; LENGTH: 305
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 US-10-363-177A-65

Query Match 98.1%; Score 20.6; DB 9; Length 305;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 31

US-10-363-177A-66
 ; Sequence 66, Application US/10363177A
 ; Publication No. US20050084851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyrosequencing AB
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
 ; APPLICANT: Ronaghi, Mostafa
 ; APPLICANT: Pourmand, Nader
 ; APPLICANT: Ekstrom, Bjorn
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
 ; FILE REFERENCE: Docket 14629
 ; CURRENT APPLICATION NUMBER: US/10/363,177A
 ; CURRENT FILING DATE: 2003-03-06
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 66
 ; LENGTH: 305
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 US-10-363-177A-66

Query Match 98.1%; Score 20.6; DB 9; Length 305;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 32

US-10-363-177A-68
 ; Sequence 68, Application US/10363177A
 ; Publication No. US20050084851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyrosequencing AB
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
 ; APPLICANT: Ronaghi, Mostafa
 ; APPLICANT: Pourmand, Nader
 ; APPLICANT: Ekstrom, Bjorn
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
 ; FILE REFERENCE: Docket 14629
 ; CURRENT APPLICATION NUMBER: US/10/363,177A
 ; CURRENT FILING DATE: 2003-03-06
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 68
 ; LENGTH: 305
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 US-10-363-177A-68

Query Match 98.1%; Score 20.6; DB 9; Length 305;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 33

US-09-345-761-6
 ; Sequence 6, Application US/09345761
 ; Patent No. US20010053518A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISHIGURO, Takahiko
 ; APPLICANT: SAITOH, Juichi
 ; APPLICANT: ISHIZUKA, Tetsuya
 ; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
 ; FILE REFERENCE: Q54969
 ; CURRENT APPLICATION NUMBER: US/09/345,761

; CURRENT FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: JP 10-186434
 ; PRIOR FILING DATE: 1998-07-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 315
 ; TYPE: DNA
 ; ORGANISM: Synthetic Construct
 US-09-345-761-6

Query Match 98.1%; Score 20.6; DB 3; Length 315;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||:|||||:|||||:|||||:
 DB 46 CCCTGTGAGGAAGTCTGTCT 66

RESULT 34
 US-10-687-588-6
 ; Sequence 6, Application US/10687588
 ; Publication No. US20040115718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISHIGURO, Takahiko
 ; APPLICANT: SAITOH, Juichi
 ; APPLICANT: ISHIZUKA, Tetsuya
 ; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
 ; FILE REFERENCE: Q54969
 ; CURRENT APPLICATION NUMBER: US/10/687,588
 ; CURRENT FILING DATE: 2003-10-20
 ; PRIOR APPLICATION NUMBER: US/09/345,761
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: JP 10-186434
 ; PRIOR FILING DATE: 1998-07-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 315
 ; TYPE: DNA
 ; ORGANISM: Synthetic Construct
 US-10-687-588-6

Query Match 98.1%; Score 20.6; DB 7; Length 315;
 Best Local Similarity 95.2%; Pred. No. 0.99;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||:|||||:|||||:|||||:
 DB 46 CCCTGTGAGGAAGTCTGTCT 66

RESULT 35
 US-09-882-945A-240
 ; Sequence 240, Application US/09882945A
 ; Publication No. US20030143535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor
 ; APPLICANT: Allawi, Hatim
 ; APPLICANT: Dong, Fang
 ; APPLICANT: Neri, Bruce
 ; APPLICANT: Vener, Tatiana
 ; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
 ; FILE REFERENCE: FORS-04586
 ; CURRENT APPLICATION NUMBER: US/09/882,945A
 ; CURRENT FILING DATE: 2001-06-15
 ; NUMBER OF SEQ ID NOS: 334
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 240
 ; LENGTH: 328
 ; TYPE: RNA
 ; ORGANISM: Hepatitis C virus

US-09-882-945A-240

Query Match 98.1%; Score 20.6; DB 3; Length 328;
 Best Local Similarity 66.7%; Pred. No. 0.99;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||:|||||:|||||:|||||:
 DB 25 CCCUGAGGAACUACUGUCU 45

RESULT 36
 US-09-882-945A-242
 ; Sequence 242, Application US/09882945A
 ; Publication No. US20030143535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor
 ; APPLICANT: Allawi, Hatim
 ; APPLICANT: Dong, Fang
 ; APPLICANT: Neri, Bruce
 ; APPLICANT: Vener, Tatiana
 ; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
 ; FILE REFERENCE: FORS-04586
 ; CURRENT APPLICATION NUMBER: US/09/882,945A
 ; CURRENT FILING DATE: 2001-06-15
 ; NUMBER OF SEQ ID NOS: 334
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 242
 ; LENGTH: 328
 ; TYPE: RNA
 ; ORGANISM: Hepatitis C virus
 US-09-882-945A-242

Query Match 98.1%; Score 20.6; DB 3; Length 328;
 Best Local Similarity 66.7%; Pred. No. 0.99;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||:|||||:|||||:|||||:
 DB 25 CCCUGAGGAACUACUGUCU 45

RESULT 37
 US-09-882-945A-243
 ; Sequence 243, Application US/09882945A
 ; Publication No. US20030143535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor
 ; APPLICANT: Allawi, Hatim
 ; APPLICANT: Dong, Fang
 ; APPLICANT: Neri, Bruce
 ; APPLICANT: Vener, Tatiana
 ; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
 ; FILE REFERENCE: FORS-04586
 ; CURRENT APPLICATION NUMBER: US/09/882,945A
 ; CURRENT FILING DATE: 2001-06-15
 ; NUMBER OF SEQ ID NOS: 334
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 243
 ; LENGTH: 328
 ; TYPE: RNA
 ; ORGANISM: Hepatitis C virus
 US-09-882-945A-243

Query Match 98.1%; Score 20.6; DB 3; Length 328;
 Best Local Similarity 66.7%; Pred. No. 0.99;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
 |||:|||||:|||||:|||||:
 DB 25 CCCUGAGGAACUACUGUCU 45

```
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-240

Query Match      98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred.No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACACTWCTGTCT 21
        |||:|||||||::|::|::|:
DB      25 CCCUGUGAGGAACUACUGUCU 45

RESULT 41
US-10-807-114-242
; Sequence 242, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 242
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-242

Query Match      98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred.No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACACTWCTGTCT 21
        |||:|||||||::|::|::|:
DB      25 CCCUGUGAGGAACUACUGUCU 45

RESULT 42
US-10-807-114-243
; Sequence 243, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
```

; SEQ ID NO 243
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-243

Query Match 98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
|||:|||||:|||||:|:|:|:
Db 25 CCUGUGAGGAACUACUGUCU 45

RESULT 43

US-10-807-114-245
; Sequence 245, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-245

Query Match 98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
|||:|||||:|||||:|:|:|:
Db 25 CCUGUGAGGAACUACUGUCU 45

RESULT 44

US-10-475-026-18
; Sequence 18, Application US/10475026
; Publication No. US20050142545A1
; GENERAL INFORMATION:
; APPLICANT: Conn, Michael Morgan
; APPLICANT: Pelligrini, Mathew
; APPLICANT: Hwang, Seongwoo
; APPLICANT: Moon, Young-choon
; APPLICANT: Almstead, Neil
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA
; FILE REFERENCE: 10389-008
; CURRENT APPLICATION NUMBER: US/10/475,026
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/282,966
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-475-026-18

Query Match 98.1%; Score 20.6; DB 9; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
|||:|||||:|||||:|:|:|:
Db 31 CCUGUGAGGAACUACUGUCU 51

RESULT 45

US-09-814-292-44
; Sequence 44, Application US/09814292
; Patent No. US20020120117A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Zhang, Hong
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 348022001500
; CURRENT APPLICATION NUMBER: US/09/814,292
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' UTR region of HCV
US-09-814-292-44

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 1;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
|||:|||||:|||||:|:|:|:
Db 43 CCCTGTGAGGAACACTGTCT 63

RESULT 46

US-09-814-357-3
; Sequence 3, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' UTR region of HCV
US-09-814-357-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 1;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGAACTWCTGTCT 21
 |||||
 Db 43 CCTGTGAGAACTACTGTCT 63

RESULT 47
 US-09-814-351-3
 ; Sequence 3, Application US/09814351
 ; Publication No. US20030148520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, De-Chao
 ; APPLICANT: Li, Yuanhao
 ; APPLICANT: Henderson, Daniel R.
 ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
 ; FILE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
 ; FILE REFERENCE: 348022001700
 ; CURRENT APPLICATION NUMBER: US/09/814,351
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/192,156
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 341
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: 5' UTR region of HCV
 US-09-814-351-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;
 Best Local Similarity 95.2%; Pred. No. 1;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGAACTWCTGTCT 21
 |||||
 Db 43 CCTGTGAGAACTACTGTCT 63

RESULT 48
 US-10-259-275-35
 ; Sequence 35, Application US/10259275
 ; Publication No. US20030125541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemon, Stanley M.
 ; APPLICANT: Yi, Minkyung
 ; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
 ; FILE REFERENCE: 265.0007 0120
 ; CURRENT APPLICATION NUMBER: US/10/259,275
 ; CURRENT FILING DATE: 2003-01-13
 ; PRIOR APPLICATION NUMBER: US 60/171,909
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: US 09/747,419
 ; PRIOR FILING DATE: 2000-12-23
 ; PRIOR APPLICATION NUMBER: US 60/325,236
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/338,123
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 35
 ; LENGTH: 341
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL
 ; FEATURE:
 ; OTHER INFORMATION: nucleotide sequence of 5' NTR
 US-10-259-275-35

Query Match 98.1%; Score 20.6; DB 6; Length 341;
 Best Local Similarity 95.2%; Pred. No. 1;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGAACTWCTGTCT 21
 |||||
 Db 43 CCTGTGAGAACTACTGTCT 63

RESULT 49
 US-10-691-045-3
 ; Sequence 3, Application US/10691045
 ; Publication No. US20040146489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, De-Chao
 ; APPLICANT: Li, Yuanhao
 ; APPLICANT: Henderson, Daniel R.
 ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
 ; FILE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
 ; FILE REFERENCE: 348022001700
 ; CURRENT APPLICATION NUMBER: US/10/691,045
 ; CURRENT FILING DATE: 2003-10-21
 ; PRIOR APPLICATION NUMBER: US/09/814,351
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/192,156
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 341
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: 5' UTR region of HCV
 US-10-691-045-3

Query Match 98.1%; Score 20.6; DB 7; Length 341;
 Best Local Similarity 95.2%; Pred. No. 1;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGAACTWCTGTCT 21
 |||||
 Db 43 CCTGTGAGAACTACTGTCT 63

RESULT 50
 US-11-006-313-35
 ; Sequence 35, Application US/11006313
 ; Publication No. US20050153281A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemon, Stanley M.
 ; APPLICANT: Yi, Minkyung
 ; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
 ; FILE REFERENCE: 265.0007 0121
 ; CURRENT APPLICATION NUMBER: US/11/006,313
 ; CURRENT FILING DATE: 2004-12-06
 ; PRIOR APPLICATION NUMBER: US 60/171,909
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: US 10/259,275
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 09/747,419
 ; PRIOR FILING DATE: 2000-12-23
 ; PRIOR APPLICATION NUMBER: US 60/325,236
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/338,123
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 35
 ; LENGTH: 341
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL
 ; FEATURE:
 ; OTHER INFORMATION: nucleotide sequence of 5' NTR
 US-11-006-313-35

Query Match 98.1%; Score 20.6; DB 10; Length 341;
 Best Local Similarity 95.2%; Pred. No. 1;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 Db 43 CCTGTGAGGAAGTCTGTCT 63

Search completed: January 27, 2006, 07:20:37
 Job time : 349.5 secs

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:38:14 ; Search time 1554.5 Seconds
(without alignments)
632.055 Million cell updates/sec

Title: US-10-070-415A-37_COPY_410_430

Perfect score: 21
Sequence: 1 gcaagtgcgtaggtgcg9999 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_hic.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_est7.*
- 9: gb_gssi.*
- 10: gb_gse2.*
- 11: gb_gse3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	92.4	516	CB151486	CB151486 K-EST0208
2	18.4	87.6	203	DR440487	DR440487 EST149_06
3	17.8	84.8	407	BF551560	BF551560 UI-R-CO-1
4	17.8	84.8	506	AJ648930	AJ648930 AJ648930
5	17.8	84.8	506	AJ648952	AJ648952 AJ648952
6	17.8	84.8	530	BG664562	BG664562 DRABPD10
7	17.8	84.8	559	BU894237	BU894237 X004H10_P
8	17.8	84.8	563	AW916775	AW916775 EST348193
9	17.8	84.8	567	CX038861	CX038861 1351947_N
10	17.8	84.8	586	CX254668	CX254668 1307434_N
11	17.8	84.8	624	CX031013	CX031013 1343080_N
12	17.8	84.8	654	BI277038	BI277038 UI-R-CYO-
13	17.8	84.8	678	CX042369	CX042369 1355939_N
14	17.8	84.8	682	BQ200617	BQ200617 UI-R-DZ1-
15	17.8	84.8	1080	BM912000	BM912000 AGENCOURT
16	17.4	82.9	488	BZ250187	BZ250187 CH230-363
17	17.4	82.9	898	BI910088	BI910088 603067926
18	17.8	81.0	529	BE235677	BE235677 143244_MA
19	17.8	81.0	535	AJ659206	AJ659206 AJ659206
20	17.8	81.0	569	CN294880	CN294880 170006000
21	17.8	81.0	574	BP455885	BP455885 BP455885
22	17.8	81.0	581	BP285205	BP285205 BP285205

C 96 16.8 80.0 979 6 CA02954 SCCCL100
 97 16.8 80.0 980 11 CNS06X0B
 98 16.8 80.0 1066 2 BE561930
 99 16.8 80.0 1192 2 BF203712
 100 16.8 80.0 1250 10 CL081883

ALIGNMENTS

RESULT 1
 CB151486
 LOCUS
 DEFINITION K-EST0208381 C1SNUL17 Homo sapiens cDNA clone C1SNUL17-33-C08 5', mRNA sequence.
 ACCESSION CB151486
 VERSION CB151486.1 GI:28135814
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 516)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Genom Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 33 row: C column: 08
 High quality sequence stop: 516.
 Location/Qualifiers
 1. .516
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C1SNUL17-33-C08"
 /sex="F"
 /tissue_type="Uterine"
 /cell_type="Epithelial"
 /cell_line="SNU-17"
 /lab_host="Top10F"
 /clone_lib="C1SNUL17"
 /note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Query Match 92.4%; Score 19.4; DB 6; Length 516;
 Best Local Similarity 95.2%; Pred. No. 2.2e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGTGTAGTGGGG 21

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 516;
 Best Local Similarity 95.2%; Pred. No. 2.2e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 63 GCAAGTGTGTAGTGGGG 83

RESULT 2
 DR440487/c

LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 PUBMED
 COMMENT

FEATURES
 source

1. .203
 /organism="Phytophthora parasitica"
 /mol_type="mRNA"
 /strain="149"
 /db_xref="taxon:4792"
 /clone="EST149_06_D12"
 /tissue_type="In vitro grown mycelium"
 /dev_stage="4 day old"
 /lab_host="VS257"
 /clone_lib="myc-149"
 /note="Vector: pBK-CNV; Site_1: EcoRI; Site_2: XhoI;
 Sample name: 1 experimental condition: rmi medium"

Query Match 87.6%; Score 18.4; DB 8; Length 203;
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

Query Match 87.6%; Score 18.4; DB 8; Length 203;
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

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 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

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 BF551560/c

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 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
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Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

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Qy 2 CAAGTGTGTAGTGGGG 21

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Qy 2 CAAGTGTGTAGTGGGG 21

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Qy 2 CAAGTGTGTAGTGGGG 21

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 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
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Qy 2 CAAGTGTGTAGTGGGG 21

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 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

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 VERSION
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 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

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 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

LOCUS
 DEFINITION

ACCESSION
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Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
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LOCUS
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Query Match 87.6%; Score 18.4; DB 8; Length 203;
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
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LOCUS
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Query Match 87.6%; Score 18.4; DB 8; Length 203;
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

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 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

LOCUS
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REFERENCE
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 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

Query Match 87.6%; Score 18.4; DB 8; Length 203;
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3
 BF551560/c

LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

Query Match 87


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/clone="C0003271_B18"
/tissue type="ovary"
/clone_lib="CSEQRAN19"
/notes="Vector: pBlueScript11(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

ORIGIN
Query Match      84.8%; Score 17.8; DB 1; Length 506;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 61 GCAAGTGCTGTAGTGGCTGTG 41

RESULT 6
BG664562/c
LOCUS      530 bp mRNA linear EST 30-APR-2001
DEFINITION DRABFD10 Rat DRG Library Rattus norvegicus cDNA clone DRABFD10 5',
mRNA sequence.
ACCESSION  BG664562
VERSION     BG664562.1 GI:13886484
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
REFERENCE  Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
AUTHORS    Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
           Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE      Identification of gene expression profile of dorsal root ganglion
           in the rat peripheral axotomy model of neuropathic pain
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
PUBMED     12060780
COMMENT    Contact: Zhang Xu
           Laboratory of Sensory System
           Institute of Neuroscience
           320 Yue Yang Road, Shanghai 200031, P.R.China
           Tel: 86-21-64748700-121
           Fax: 86-21-64713446
           Email: xu.zhang@ion.ac.cn
           This clone is also available at Chinese National Human Genome
           Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
           Pudong New Area, P.R.China. Please contact with Zhang Xu
           (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
PolyA=No.

FEATURES
source      Location/Qualifiers
1..530
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRABFD10"
/sex="male"
/tissue type="dorsal root ganglion"
/dev stage="adult"
/clone_lib="Rat DRG Library"

ORIGIN
Query Match      84.8%; Score 17.8; DB 2; Length 530;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||

```

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Db 85 GCAAGTGCTGTAGTGGCTGTG 65

RESULT 7
BUB94237
LOCUS      559 bp mRNA linear EST 17-OCT-2002
DEFINITION X004H10 Populus wood cDNA library Populus tremula x Populus
tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION  BUB94237
VERSION     BUB94237.1 GI:24105302
KEYWORDS   EST.
SOURCE     Populus tremula x Populus tremuloides
ORGANISM   Populus tremula x Populus tremuloides
REFERENCE  1 (bases 1 to 559)
AUTHORS    Unneberg,P., Bhallerao,R.R., Jansson,S. and Sterky,F.
TITLE      The poplar tree transcriptome: Analysis of expressed sequence tags
           from multiple libraries
JOURNAL    Unpublished (2002)
COMMENT    Contact: BHALLERAO RUPALI R.
           Umea Plant Science Center
           Department of Plant Physiology
           University of Umea, 901 87 Umea, Sweden
           Tel: +46 90 786 5279
           Fax: +46 90 786 6676
           Email: rupali.bhallerao@plantphys.umu.se.

FEATURES
source      Location/Qualifiers
1..559
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue type="wood"
/clone_lib="Populus wood cDNA library"

ORIGIN
Query Match      84.8%; Score 17.8; DB 5; Length 559;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21
|||||
Db 465 GCAAGTGATGAGGTGCGGG 485

RESULT 8
AW916775/c
LOCUS      563 bp mRNA linear EST 25-MAY-2000
DEFINITION EST348183 Rat gene index, normalized rat, norvegicus, Bento Soares
Rattus norvegicus cDNA clone RG1DW15 5' end, mRNA sequence.
ACCESSION  AW916775
VERSION     AW916775.1 GI:8082615
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
           Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
           Kerlavage,A.R. and Adams,M.D.
TITLE      Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
           Gene Index
JOURNAL    Unpublished (1998)
COMMENT    Contact: Lee, NH
           The Institute for Genomic Research
           9712, Medical Center Drive, Rockville, MD 20850, USA
           Tel: (301)-838-3529
           Fax: (301)-838-0208
           Email: nhlee@tigr.org
           This clone is available through the ATCC, contact the ATCC
           tel#703-365-2700 for further information

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LOCUS
DEFINITION 1307434 NCCWA 02RT Oncorhynchus mykiss cdna 3', mRNA sequence.
ACCESSION CX254668
VERSION CX254668.1 GI:60371200
KEYWORDS EST.
SOURCE
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 586)
Rexroad, C.E., Goupil, A.-S., Guiguen, Y. and Yao, J.
02RT IUS, NCCWA/WVU EST Project, Phase II, in collaboration with
INRA
Unpublished (2004)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 115 row: K column: 15
Seq primer: GTAATACGACTCACTATAGG.
FEATURES             source
     1..586
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /tissue_type="pooled"
     /lab_host="DH10B"
     /clone_lib="NCCWA 02RT"
     /note="Vector: pCMV Sport6.0; This library was created by
A.-S. Goupil and Y. Guiguen who subtracted the NCCWA 1RT
library from the INRA multi-tissue library."
ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 586;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGGG 21
    ||| ||||| ||||| |||||
Db 530 GCTAGGCTGTAGGTGCGGG 550

RESULT 11
LOCUS CX031013/c
DEFINITION 1343080 NCCWA 10RT#3 Oncorhynchus mykiss cdna 5', mRNA sequence.
ACCESSION CX031013
VERSION CX031013.1 GI:56975367
KEYWORDS EST.
SOURCE
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 624)
Yao, J., Gahr, S. and Rexroad, C.E.
10RT#3 egg, NCCWA/WVU EST Project, Phase II
Unpublished (2004)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 143 row: P column: 9
Seq primer: GTAATACGACTCACTATAGG.
FEATURES             source
     1..567
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /lab_host="DH10B"
     /clone_lib="NCCWA 10RT#3"
     /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."
ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 567;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGGG 21
    ||| ||||| ||||| |||||
Db 40 GCTAGGCTGTAGGTGCGGG 20

RESULT 9
CX038861/c
LOCUS CX038861
DEFINITION 1351947 NCCWA 10RT#3 Oncorhynchus mykiss cdna 5', mRNA sequence.
ACCESSION CX038861
VERSION CX038861.1 GI:56983215
KEYWORDS EST.
SOURCE
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 567)
Yao, J., Gahr, S. and Rexroad, C.E.
10RT#3 egg, NCCWA/WVU EST Project, Phase II
Unpublished (2004)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 143 row: P column: 9
Seq primer: GTAATACGACTCACTATAGG.
FEATURES             source
     1..567
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /lab_host="DH10B"
     /clone_lib="NCCWA 10RT#3"
     /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."
ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 567;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGGG 21
    ||| ||||| ||||| |||||
Db 40 GCTAGGCTGTAGGTGCGGG 20

RESULT 10
CX254668
LOCUS CX254668
DEFINITION 1307434 NCCWA 02RT Oncorhynchus mykiss cdna 3', mRNA sequence.
ACCESSION CX254668
VERSION CX254668.1 GI:60371200
KEYWORDS EST.
SOURCE
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 586)
Rexroad, C.E., Goupil, A.-S., Guiguen, Y. and Yao, J.
02RT IUS, NCCWA/WVU EST Project, Phase II, in collaboration with
INRA
Unpublished (2004)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 115 row: K column: 15
Seq primer: GTAATACGACTCACTATAGG.
FEATURES             source
     1..586
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /tissue_type="pooled"
     /lab_host="DH10B"
     /clone_lib="NCCWA 02RT"
     /note="Vector: pCMV Sport6.0; This library was created by
A.-S. Goupil and Y. Guiguen who subtracted the NCCWA 1RT
library from the INRA multi-tissue library."
ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 586;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGGG 21
    ||| ||||| ||||| |||||
Db 530 GCTAGGCTGTAGGTGCGGG 550

RESULT 11
LOCUS CX031013/c
DEFINITION 1343080 NCCWA 10RT#3 Oncorhynchus mykiss cdna 5', mRNA sequence.
ACCESSION CX031013
VERSION CX031013.1 GI:56975367
KEYWORDS EST.
SOURCE
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 624)
Yao, J., Gahr, S. and Rexroad, C.E.
10RT#3 egg, NCCWA/WVU EST Project, Phase II
Unpublished (2004)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 143 row: P column: 9
Seq primer: GTAATACGACTCACTATAGG.
FEATURES             source
     1..567
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /lab_host="DH10B"
     /clone_lib="NCCWA 10RT#3"
     /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."
ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 567;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGGG 21
    ||| ||||| ||||| |||||
Db 40 GCTAGGCTGTAGGTGCGGG 20

RESULT 9
CX038861/c
LOCUS CX038861
DEFINITION 1351947 NCCWA 10RT#3 Oncorhynchus mykiss cdna 5', mRNA sequence.
ACCESSION CX038861
VERSION CX038861.1 GI:56983215
KEYWORDS EST.
SOURCE
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 567)
Yao, J., Gahr, S. and Rexroad, C.E.
10RT#3 egg, NCCWA/WVU EST Project, Phase II
Unpublished (2004)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 143 row: P column: 9
Seq primer: GTAATACGACTCACTATAGG.
FEATURES             source
     1..567
     /organism="Oncorhynchus mykiss"
     /mol_type="mRNA"
     /db_xref="taxon:8022"
     /lab_host="DH10B"
     /clone_lib="NCCWA 10RT#3"
     /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."
ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 567;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGGTGCGGG 21
    ||| ||||| ||||| |||||
Db 40 GCTAGGCTGTAGGTGCGGG 20

RESULT 10
CX254668
LOCUS CX254668
DEFINITION
```

Plate: 119 row: F column: 22
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers
 1. .624
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /lab_host="DH10B"
 /clone_lib="NCCWA 10RT#3"
 /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."

FEATURES
 source

ORIGIN
 Query Match 84.8%; Score 17.8; DB 8; Length 624;
 Best Local Similarity 90.5%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 |||
 Db 374 GCTAGGCTGTAGTGGGGG 354

RESULT 12
 LOCUS BI277038 654 bp mRNA linear EST 19-JUL-2001
 DEFINITION UI-R-CYO-bxp-g-02-0-UI.s1 UI-R-CYO Rattus norvegicus cDNA clone
 ACCESSION UI-R-CYO-bxp-g-02-0-UI 3', mRNA sequence.
 VERSION BI277038.1 GI:14922529
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 654)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized brown adipose library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.regen.com).
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 source
 1. .654
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CYO-bxp-g-02-0-UI"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CYO"

note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CYO library is a non-normalized library constructed from rat brown adipose tissue. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has

ORIGIN
 Query Match 84.8%; Score 17.8; DB 8; Length 624;
 Best Local Similarity 90.5%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 |||
 Db 443 GCTAGGCTGTAGTGGGGG 423

RESULT 14
 LOCUS BQ200617 682 bp mRNA linear EST 12-AUG-2004
 DEFINITION UI-R-DZ1-cne-k-16-0-UI.s1 NCI CGAP_D21 Rattus norvegicus cDNA clone
 ACCESSION BQ200617.1 GI:20417082
 VERSION BQ200617.1
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 678)
 AUTHORS Yoo,J., Gahr,S. and Rexroad,C.F.
 TITLE 10RT#3 egg, NCCWA/WVU EST Project, Phase II
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
 Plate: 154 row: F column: 17
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers
 1. .678
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /lab_host="DH10B"
 /clone_lib="NCCWA 10RT#3"
 /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."

been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_TISSUE=brown adipose
 TAG_LIB=UI-R-CYO
 TAG_SEQ=TTGTC"

ORIGIN
 Query Match 84.8%; Score 17.8; DB 2; Length 654;
 Best Local Similarity 90.5%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 |||
 Db 628 GCAAGTGTCTAGTGGCTGTG 648

RESULT 13
 LOCUS CX042369/c 678 bp mRNA linear EST 03-JAN-2005
 DEFINITION 1355939 NCCWA 10RT#3 Oncorhynchus mykiss cDNA 5', mRNA sequence.
 ACCESSION CX042369
 VERSION CX042369.1 GI:56986723
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss

REFERENCE 1 (bases 1 to 678)
 AUTHORS Yoo,J., Gahr,S. and Rexroad,C.F.
 TITLE 10RT#3 egg, NCCWA/WVU EST Project, Phase II
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
 Plate: 154 row: F column: 17
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers
 1. .678
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /lab_host="DH10B"
 /clone_lib="NCCWA 10RT#3"
 /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."

ORIGIN
 Query Match 84.8%; Score 17.8; DB 8; Length 678;
 Best Local Similarity 90.5%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 |||
 Db 443 GCTAGGCTGTAGTGGGGG 423

RESULT 14
 LOCUS BQ200617 682 bp mRNA linear EST 12-AUG-2004
 DEFINITION UI-R-DZ1-cne-k-16-0-UI.s1 NCI CGAP_D21 Rattus norvegicus cDNA clone
 ACCESSION BQ200617.1 GI:20417082
 VERSION BQ200617.1
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 678)
 AUTHORS Yoo,J., Gahr,S. and Rexroad,C.F.
 TITLE 10RT#3 egg, NCCWA/WVU EST Project, Phase II
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
 Plate: 154 row: F column: 17
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers
 1. .678
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /lab_host="DH10B"
 /clone_lib="NCCWA 10RT#3"
 /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."

ORIGIN
 Query Match 84.8%; Score 17.8; DB 8; Length 678;
 Best Local Similarity 90.5%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGGG 21
 |||
 Db 443 GCTAGGCTGTAGTGGGGG 423

RESULT 14
 LOCUS BQ200617 682 bp mRNA linear EST 12-AUG-2004
 DEFINITION UI-R-DZ1-cne-k-16-0-UI.s1 NCI CGAP_D21 Rattus norvegicus cDNA clone
 ACCESSION BQ200617.1 GI:20417082
 VERSION BQ200617.1
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 678)
 AUTHORS Yoo,J., Gahr,S. and Rexroad,C.F.
 TITLE 10RT#3 egg, NCCWA/WVU EST Project, Phase II
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
 Plate: 154 row: F column: 17
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers
 1. .678
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /lab_host="DH10B"
 /clone_lib="NCCWA 10RT#3"
 /note="Vector: pCMV Sport6.0; WVU oocyte library RT-EGG."

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 682)

AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

PUBMED

8889548

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Oligo-dr track not found, Not 1 site shown in beginning of sequence

is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

IMAGE (<http://image.llnl.gov>)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

Location/Qualifiers

1..682

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="IMAGE:7344618"

/tissue_type="Chondrosarcoma"

/dev_stage="37 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP_D21"

/note="Organ: Spine; Vector: p7T3D-Pac (Pharmacia) with a

modified polylinker; Site 1: Not 1; Site 2: Eco RI;

UI-R-D21 is a normalized cDNA library containing the

following tissue(s): Swarm Rat Chondrosarcoma. The library

was constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dr primer containing a

Not 1 site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not 1, and cloned directionally

into p7T3-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not 1 site and the

(dT)18 tail. The sequence tag for this library is

CATTCTTGTA. The rat cartilaginous tumor tissue was

provided by Dr Jeff Stevens at the University of Iowa.

TAG TISSUE=cartilaginous tumor

TAG_LIB=UI-R-D21

TAG_SEQ=CATTCTTGTA"

ORIGIN

Query Match

Best Local Similarity 84.8%; Score 17.8; DB 3; Length 682;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 GCAAGTGTCTAGTGTGGGG 21

Db

608 GCAAGTGTCTAGTGTCTGTG 628

RESULT 15

BM912000/c

LOCUS

DEFINITION AGENCOURT 6613112 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5473480

5', mRNA sequence.

ACCESSION

BM912000

VERSION

BM912000.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1080)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LICM1985 row: c column: 17

High quality sequence stop: 531.

FEATURES

Location/Qualifiers

1..1080

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5473480"

/tissue_type="amelanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC_41"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 84.8%; Score 17.8; DB 3; Length 1080;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 GCAAGTGTCTAGTGTGGGG 21

Db

711 GCAATTGTGTGGTGGGG 691

RESULT 16

BZ250187

LOCUS

DEFINITION

BZ250187

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 488)

Zhao, S., Shetty, J., Shatsman, S., Tsengave, G., Geer, K.,

Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,

Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 MboI segment

Unpublished (1999)

Other GSSs: CH230-363D18.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomes

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rac230.htm>). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end
 page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
 Plate: 363 row: D column: 18

Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..488
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SsNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-363D18"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 488;
 Best Local Similarity 94.7%; Pred. No. 2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGTCTGTAGTGGCGG 20
 |||||
 Db 2 CAAGTCTGTAGTGGCGG 20

RESULT 17

BI910088 898 bp mRNA linear EST 16-OCT-2001
 LOCUS 603067926F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216958 5',
 DEFINITION mRNA sequence.

ACCESSION BI910088
 VERSION BI910088.1 GI:16173428

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 898)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LHAM1545 row: C column: 07

High quality sequence stop: 779.

Location/Qualifiers

1..898
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5216958"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_118"
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber

FEATURES

source

Query Match 81.0%; Score 17; DB 2; Length 529;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGG 21
 |||||

Db 192 GTGCTGTAGTGGCGG 176

RESULT 19

AJ659206 535 bp mRNA linear EST 28-JUN-2004
 LOCUS AJ659206/c
 DEFINITION AJ659206 KN277 Sus scrofa cDNA clone C0005215_I12, mRNA sequence.

(Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 82.9%; Score 17.4; DB 3; Length 898;
 Best Local Similarity 94.7%; Pred. No. 2.1e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CAAGTCTGTAGTGGCGG 20
 |||||
 Db 531 CAAGTCTGTAGTGGCGG 549

RESULT 19

BE235677/c 529 bp mRNA linear EST 10-JUL-2000
 LOCUS 143244 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION BE235677
 ACCESSION BE235677
 VERSION BE235677.1 GI:9020395

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 529)
 AUTHORS Fahrkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
 Vallet,J., Wise,T., Rohrer,G.A., Perlea,G., Sultana,R.,
 Quackenbush,J. and Keeler,J.W.
 TITLE Porcine gene discovery by normalized cDNA-library sequencing and
 EST cluster assembly
 JOURNAL Mamm. Genome 13 (8), 475-478 (2002)
 PUBMED 12226715
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

Plate: 84 row: K column: 8

Seq primer: ATTAGTGACACTATAG.

Location/Qualifiers

1..529
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 1P1G"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."

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ACCESSION AJ659206
VERSION AJ659206.1 GI:49343337
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

1 (bases 1 to 535)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by crossmatch with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.

FEATURES             Location/Qualifiers
     source           1..535
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0005215_112"
                     /tissue_type="embryo"
                     /clone_lib="KN277"
                     /note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pooled early embryos, from 8-cell stage
                     to blastocysts."

ORIGIN
Query Match      81.0%; Score 17; DB 1; Length 535;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGC GGCGG 21
    |||||||
Db 45 GTGCTGTAGTGC GGCGG 29

RESULT 20
CN294880/c
LOCUS CN294880.1 569 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700600093822 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN294880
VERSION CN294880.1 GI:47311294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 569)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658

FEATURES             Location/Qualifiers
     source           1..569
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, DMSO-treated H9 cell
                     line"
                     /clone_lib="GRN_PREHEP"
                     /note="oligo dt primed, full-length enriched cDNA library
                     from DMSO-treated hES cell line H9 (p22) maintained in
                     feeder-free conditions"

ORIGIN
Query Match      81.0%; Score 17; DB 7; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGC GGCGG 21
    |||||||
Db 548 GTGCTGTAGTGC GGCGG 532

RESULT 21
BP455885/c
LOCUS BP455885 574 bp mRNA linear EST 31-DEC-2003
DEFINITION BP455885 full-length enriched swine cDNA library, adult ovary Sus
scrofa cDNA clone OVRM10038B05 5', mRNA sequence.
ACCESSION BP455885
VERSION BP455885.1 GI:40467400
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 574)
Unishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamasima, N. and Awata, T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
14681463
Contact: Hirohide Unishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES             Location/Qualifiers
     source           1..574
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="OVRM10038B05"
                     /tissue_type="ovary"
                     /dev stage="adult"
                     /clone_lib="full-length enriched swine cDNA library, adult
                     ovary"

ORIGIN
Query Match      81.0%; Score 17; DB 3; Length 574;

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Best Local Similarity 100.0%; Pred. No. 3.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
|||||
Db 574 GTGCTGTAGTGGGGG 558

RESULT 22
BP285205/c
LOCUS
DEFINITION
581 bp mRNA linear EST 16-SEP-2004
BP285205 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL01254, mRNA sequence.
ACCESSION
BP285205
VERSION
BP285205.1 GI:52198937
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..581
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL01254"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
Query Match 81.0%; Score 17; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21
|||||
Db 568 GTGCTGTAGTGGGGG 552

RESULT 24
BP288316/c
LOCUS
DEFINITION
581 bp mRNA linear EST 16-SEP-2004
BP288316 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL08636, mRNA sequence.
ACCESSION
BP288316
VERSION
BP288316.1 GI:52202048
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..581
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL01254"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
Query Match 81.0%; Score 17; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21
|||||
Db 567 GTGCTGTAGTGGGGG 551

RESULT 23
BP288204/c
LOCUS
DEFINITION
581 bp mRNA linear EST 16-SEP-2004
BP288204 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL08345, mRNA sequence.
ACCESSION
BP288204
VERSION
BP288204.1 GI:52201936
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
```

```
15342556
PUBMED
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL08345"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
Query Match 81.0%; Score 17; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21
|||||
Db 571 GTGCTGTAGTGGGGG 555

RESULT 24
BP288316/c
LOCUS
DEFINITION
581 bp mRNA linear EST 16-SEP-2004
BP288316 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL08636, mRNA sequence.
ACCESSION
BP288316
VERSION
BP288316.1 GI:52202048
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL08636"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
Query Match 81.0%; Score 17; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21
|||||
Db 571 GTGCTGTAGTGGGGG 555
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RESULT 25
BP251402/c
LOCUS
DEFINITION
  BP251402 Sugano cDNA library, 582 bp mRNA linear EST 15-SEP-2004
  HPR07515, mRNA sequence.
ACCESSION
  BP251402
VERSION
  BP251402.1 GI:52133683
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 (bases 1 to 582)
  Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
  Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  Sequence comparison of human and mouse genes reveals a homologous
  block structure in the promoter regions
  Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
  PUBMED
COMMENT
  Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
  source
  1..582
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /tissue_type="hippocampus"
  /clone_lib="Sugano cDNA library, hippocampus"
ORIGIN
  Query Match 81.0%; Score 17; DB 3; Length 582;
  Best Local Similarity 100.0%; Pred.No. 3.1e+03;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 5 GTGCTGTAGTGGCGGG 21
  Db 496 GTGCTGTAGTGGCGGG 480
  |||||
  RESULT 26
  BP285843/c
  LOCUS
  DEFINITION
    BP285843 Sugano cDNA library, 582 bp mRNA linear EST 16-SEP-2004
    clone LFL02931, mRNA sequence.
  ACCESSION
    BP285843
  VERSION
    BP285843.1 GI:52199575
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  REFERENCE
    1 (bases 1 to 582)
    Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
    Mizushima-Sugano,J., Nakai,K. and Sugano,S.
    Sequence comparison of human and mouse genes reveals a homologous
    block structure in the promoter regions
    Genome Res. 14 (9), 1711-1718 (2004)
  JOURNAL
    PUBMED
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp.
  FEATURES
    source
    1..582
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /tissue_type="lung"
    /clone_lib="Sugano cDNA library, lung fibroblast"
ORIGIN
  Query Match 81.0%; Score 17; DB 3; Length 582;
  Best Local Similarity 100.0%; Pred.No. 3.1e+03;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 5 GTGCTGTAGTGGCGGG 21
  Db 496 GTGCTGTAGTGGCGGG 480
  |||||
  RESULT 27
  BP285880/c
  LOCUS
  DEFINITION
    BP285880 Sugano cDNA library, 582 bp mRNA linear EST 16-SEP-2004
    clone LFL02985, mRNA sequence.
  ACCESSION
    BP285880
  VERSION
    BP285880.1 GI:52199612
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  REFERENCE
    1 (bases 1 to 582)
    Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
    Mizushima-Sugano,J., Nakai,K. and Sugano,S.
    Sequence comparison of human and mouse genes reveals a homologous
    block structure in the promoter regions
    Genome Res. 14 (9), 1711-1718 (2004)
  JOURNAL
    PUBMED
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp.
  FEATURES
    source
    1..582
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone_lib="Sugano cDNA library, lung fibroblast"
ORIGIN
  Query Match 81.0%; Score 17; DB 3; Length 582;
  Best Local Similarity 100.0%; Pred.No. 3.1e+03;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 5 GTGCTGTAGTGGCGGG 21
  Db 574 GTGCTGTAGTGGCGGG 558
  |||||
  RESULT 28
  BP286155/c
  LOCUS
  DEFINITION
    BP286155 Sugano cDNA library, 582 bp mRNA linear EST 16-SEP-2004
    clone LFL03540, mRNA sequence.
  ACCESSION
    BP286155
  VERSION
    BP286155.1 GI:52199887
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  REFERENCE
    1 (bases 1 to 582)
    Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
    Mizushima-Sugano,J., Nakai,K. and Sugano,S.
    Sequence comparison of human and mouse genes reveals a homologous
    block structure in the promoter regions
    Genome Res. 14 (9), 1711-1718 (2004)
  JOURNAL
    PUBMED
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp.
  FEATURES
    source
    1..582
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /tissue_type="lung"
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  QY 5 GTGCTGTAGTGGCGGG 21
  Db 571 GTGCTGTAGTGGCGGG 555
  |||||
  RESULT 29
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  LOCUS
  DEFINITION
    BP286155 Sugano cDNA library, 582 bp mRNA linear EST 16-SEP-2004
    clone LFL03540, mRNA sequence.
  ACCESSION
    BP286155
  VERSION
    BP286155.1 GI:52199887
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  REFERENCE
    1 (bases 1 to 582)
    Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
    Mizushima-Sugano,J., Nakai,K. and Sugano,S.
    Sequence comparison of human and mouse genes reveals a homologous
    block structure in the promoter regions
    Genome Res. 14 (9), 1711-1718 (2004)
  JOURNAL
    PUBMED
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp.
  FEATURES
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    1..582
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
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ORIGIN
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  Best Local Similarity 100.0%; Pred.No. 3.1e+03;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 5 GTGCTGTAGTGGCGGG 21
  Db 571 GTGCTGTAGTGGCGGG 555
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
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Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
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/db_xref="taxon:9606"
/clone="LFL03540"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 571 GTGCTGTAGTGGCGGG 555

RESULT 29
BP286331/c
LOCUS
DEFINITION
BP286331 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL03946, mRNA sequence.
ACCESSION
BP286331
VERSION
BP286331.1 GI:52200663
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
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Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

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/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

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QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 571 GTGCTGTAGTGGCGGG 555

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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 570 GTGCTGTAGTGGCGGG 554

RESULT 30
BP287184/c
LOCUS
DEFINITION
BP287184 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL05920, mRNA sequence.
ACCESSION
BP287184
VERSION
BP287184.1 GI:52200916
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
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Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

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/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
Query Match 81.0%; Score 17; DB 3; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 570 GTGCTGTAGTGGCGGG 554

RESULT 31
BP287610/c
LOCUS
DEFINITION
BP287610 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL07025, mRNA sequence.
ACCESSION
BP287610
VERSION
BP287610.1 GI:52201342
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL
PUBMED
COMMENT

Genome Res. 14 (9), 1711-1718 (2004)
15342556
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Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

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ORIGIN

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 545 GTGCTGTAGTGGCGGG 529

RESULT 32

BP354534/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BP354534 582 bp mRNA linear EST 17-SEP-2004
BP354534 Sugano cDNA library, squamous cell TE7 Homo sapiens cDNA
clone T7R04243, mRNA sequence.

BP354534

BP354534.1

GI:52284520

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 582)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

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Location/Qualifiers

1. .582

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="T7R04243"

/cell_type="squamous cell"

/cell_line="TE7"

/clone_lib="Sugano cDNA library, squamous cell TE7"

/note="squamous cell carcinoma"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 573 GTGCTGTAGTGGCGGG 557

RESULT 33

BP359182/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BP359182 582 bp mRNA linear EST 17-SEP-2004
BP359182 Sugano cDNA library, mammary gland T47D Homo sapiens cDNA
clone TDR08082, mRNA sequence.

BP359182

BP359182.1

GI:52289195

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 582)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

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Location/Qualifiers

1. .582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TDR08082"

/tissue_type="mammary gland"

/cell_line="T47D"

/clone_lib="Sugano cDNA library, mammary gland T47D"

/note="mammary gland tumor"

ORIGIN

Query Match 81.0%; Score 17; DB 3; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 571 GTGCTGTAGTGGCGGG 555

RESULT 34

BP285644/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BP285644 583 bp mRNA linear EST 16-SEP-2004
BP285644 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL02445, mRNA sequence.

BP285644

BP285644.1

GI:52199376

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 583)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

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Location/Qualifiers

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 GTGCTGTAGTGGCGGG 21
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Db  570 GTGCTGTAGTGGCGGG 554

RESULT 35
BP286330/c
LOCUS
DEFINITION
BP286330 Sugano cDNA library, lung fibroblast Homo sapiens CDNA
clone LFL03941, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
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AUTHORS
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
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block structure in the promoter regions
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15342556
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

JOURNAL
PUBMED
COMMENT

FEATURES
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/notes="normal"

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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 GTGCTGTAGTGGCGGG 21
|||||
Db  571 GTGCTGTAGTGGCGGG 555

RESULT 36
BP287530/c
LOCUS
DEFINITION
BP287530 Sugano cDNA library, lung fibroblast Homo sapiens CDNA
clone LFL06826, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
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Email: yusuzuki@ims.u-tokyo.ac.jp.

AUTHORS
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Mizushima-Sugano, J., Nakai, K. and Sugano, S.
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15342556
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Email: yusuzuki@ims.u-tokyo.ac.jp.

JOURNAL
PUBMED
COMMENT

FEATURES
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1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/notes="normal"

ORIGIN
Query Match      81.0%; Score 17; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 GTGCTGTAGTGGCGGG 21
|||||
Db  571 GTGCTGTAGTGGCGGG 555

RESULT 36
BP287530/c
LOCUS
DEFINITION
BP287530 Sugano cDNA library, lung fibroblast Homo sapiens CDNA
clone LFL06826, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
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15342556
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Email: yusuzuki@ims.u-tokyo.ac.jp.

AUTHORS
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block structure in the promoter regions
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15342556
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Email: yusuzuki@ims.u-tokyo.ac.jp.

JOURNAL
PUBMED
COMMENT

FEATURES
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1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
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/notes="normal"

ORIGIN

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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
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Genome Res. 14 (9), 1711-1718 (2004)
15342556
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
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AUTHORS
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block structure in the promoter regions
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15342556
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Email: yusuzuki@ims.u-tokyo.ac.jp.

JOURNAL
PUBMED
COMMENT

FEATURES
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1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN
Query Match      81.0%; Score 17; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 GTGCTGTAGTGGCGGG 21
|||||
Db  572 GTGCTGTAGTGGCGGG 556

RESULT 37
BP342212/c
LOCUS
DEFINITION
BP342212 Sugano cDNA library, stomach mucosa Homo sapiens cDNA
clone STM04411, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

AUTHORS
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Mizushima-Sugano, J., Nakai, K. and Sugano, S.
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block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
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Email: yusuzuki@ims.u-tokyo.ac.jp.

JOURNAL
PUBMED
COMMENT

FEATURES
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1. .583
/organism="Homo sapiens"
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ORIGIN

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Query Match 81.0%; Score 17; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 571 GTGCTGTAGTGGCGGG 555

RESULT 38
CA406235/c
LOCUS CA406235 603 bp mRNA linear EST 07-NOV-2002
DEFINITION cDNA 5'-Stretch Plus cDNA Library Homo sapiens
CDNA 5', mRNA sequence.
ACCESSION CA406235
VERSION CA406235.1 GI:24771106
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 603)
AUTHORS Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
TITLE EST analysis of human adipose gene expression
JOURNAL Unpublished (2002)
COMMENT Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St., HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGAGCGCGCCATTGTGTGGT
BACKWARD: AATGACTACTATAGGCGGAATTG
Seq primer: GTTGGTACCCGGGAATTC.
Location/Qualifiers
1. .603
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Male and Female"
/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplex"

ORIGIN

Query Match 81.0%; Score 17; DB 6; Length 603;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 537 GTGCTGTAGTGGCGGG 521

RESULT 39
BP336613/c
LOCUS BP336613 611 bp mRNA linear EST 17-SEP-2004
DEFINITION BP336613 Sugano cDNA library, coronary artery smooth muscle cell
Homo sapiens cDNA clone SMR06107, mRNA sequence.
ACCESSION BP336613
VERSION BP336613.1 GI:52266194
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 611)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. .611
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SMR06107"
/tissue_type="coronary artery"
/cell_type="smooth muscle cell"
/clone_lib="Sugano cDNA library, coronary artery smooth
muscle cell"

ORIGIN

Query Match 81.0%; Score 17; DB 3; Length 611;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
|||||
Db 570 GTGCTGTAGTGGCGGG 554

RESULT 40
AU128757/c
LOCUS AU128757 633 bp mRNA linear EST 01-AUG-2002
DEFINITION AU128757 NT2RP2 Homo sapiens cDNA clone NT2RP2004133 5', mRNA
sequence.
ACCESSION AU128757
VERSION AU128757.1 GI:10989111
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 633)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2004133"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

```

Query Match      81.0%; Score 17; DB 1; Length 633;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
    |||||
DB 572 GTGCTGTAGTGGCGGG 556

RESULT 41
CJ006547/c
LOCUS
DEFINITION
  CJ006547 full-length enriched swine cDNA library, adult liver Sus
  scrofa cDNA clone LVRM1H010194 5', mRNA sequence.
ACCESSION
  CJ006547
VERSION
  CJ006547.1 GI:54495372
KEYWORDS
  EST.
SOURCE
  Sus scrofa (pig)
ORGANISM
  Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
  Sus.
REFERENCE
  1 (bases 1 to 633)
AUTHORS
  Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
  Okumura,N., Hamasima,N. and Awata,T.
TITLE
  PEDE (Pig EST Data Explorer): construction of a database for ESTs
  derived from porcine full-length cDNA libraries
JOURNAL
  Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED
  14681463
COMMENT
  Contact: Hirohide Uenishi
  Animal Genome Laboratory, Genome Research Department
  National Institute of Agrobiological Sciences
  2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
  Tel: +81-29-838-8627
  Fax: +81-29-838-8627
  Email: huenishi@affrc.go.jp
  EST project with full-length enriched cDNA libraries carried out in
  Animal Genome Research Program (Japan) by National Institute of
  Agrobiological Sciences and STAFF-Institute
  Single pass sequencing of clones derived from oligo-capped cDNA
  library
  Vector sequences were eliminated by RepeatMasker version 2002/07/13
  and crossmatch version 0.990319
  Low quality bases were trimmed based on the quality values.
FEATURES
  source
    1..633
    /organism="Sus scrofa"
    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /clones="LVRM1H010194"
    /tissue_type="liver"
    /dev_stage="adult"
    /clone_lib="full-length enriched swine cDNA library, adult
    liver"

ORIGIN
Query Match      81.0%; Score 17; DB 7; Length 633;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
    |||||
DB 574 GTGCTGTAGTGGCGGG 558

RESULT 42
CN484921/c
LOCUS
DEFINITION
  hx20f09.y1 Human primary human ocular pericytes. Equalized (hx)
  Homo sapiens cDNA clone hx20f09 5', mRNA sequence.
ACCESSION
  CN484921
VERSION
  CN484921.1 GI:46566425

KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1 (bases 1 to 638)
AUTHORS
  Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
  Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,

KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1 (bases 1 to 638)
AUTHORS
  Tsai,J.Y. and Wistow,G.
  Expressed sequence tag analysis of cultured primary human ocular
  pericytes
  Unpublished (2004)
JOURNAL
  Contact: Wistow G
  Section on Molecular Structure and Function
  National Eye Institute
  6/331, NIH, Bethesda, MD 20892-2740, USA
  Tel: 301 402 3452
  Fax: 301 496 0078
  Email: graeme@helix.nih.gov
  Plate: 20 row: f column: 09
  Seq primer: M3RP1 reverse primer (ABI).
  Location/Qualifiers
    1..638
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="hx20f09"
    /cell_type="pericytes"
    /dev_stage="Adult"
    /lab_host="EMDH10B"
    /clone_lib="Human primary human ocular pericytes.
    Equalized (hx)"
    /note="Organ: Eye; Vector: pSPORT1; RNA was extracted from
    primary human pericytes in culture. A directionally cloned
    cDNA library in the pSPORT1 vector (Invitrogen) was
    constructed at Bioserve Biotechnology (Laurel MD)
    essentially following the protocols of the SuperScript
    Plasmid System full details of which are contained in the
    manufacturer's instruction manual
    (http://www.lifetech.com/). First strand synthesis was
    carried out using a Not I primer-adaptor
    (5'-pGACTAGTTCTAGATCGGCGGCCG(T)15-3'). cDNA was
    cloned in Not I/Sal I sites. EST analysis was performed at
    the NIH Intramural Sequencing Center (NISC). This library
    is derived from the original unamplified library and
    subjected to equalization to reduce occurrence of abundant
    clones."
ORIGIN
Query Match      81.0%; Score 17; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
    |||||
DB 508 GTGCTGTAGTGGCGGG 492

RESULT 43
CV029040/c
LOCUS
DEFINITION
  CV029040 638 bp mRNA linear EST 20-AUG-2004
  sapiens cDNA 5' similar to BC014454, mRNA sequence.
ACCESSION
  CV029040
VERSION
  CV029040.1 GI:51487171
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1 (bases 1 to 638)
AUTHORS
  Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
  Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,

```

Clingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
 Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
 Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
 Human ORFeome Version 1.1: a Platform for Reverse Proteomics
 Genome Res. (2004) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu

TITLE
 JOURNAL
 COMMENT

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
 results from a PCR reaction using an MGC full-length cDNA as
 template DNA and ORF specific primers
 PCR Primers
 FORWARD: ATGGGGGAACACAGTCCAGACAA
 BACKWARD: CACTTGGAGAGCTGCTGGTGA
 Insert Length: 638 Std Error: 41.00
 Plate: 11078 row: 05 column: A
 Seq primer: ACTGGCGCTGTTTACAACTGCTGACTGGGAAAC
 High quality sequence start: 101
 High quality sequence stop: 637
 POLYA=No.

FEATURES
 source

1..638 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="mixed"
 /clone_lib="Full length cDNA from the Mammalian Gene
 Collection"

/note="Vector: mixed; The ORFs were PCR amplified from the
 MGC (Mammalian Gene Collection) as of April 2004 and
 cloned by recombinational Gateway cloning into pDONR223
 Donor vector. Reference : MGC (Mammalian Gene Collection)
 Program Team, Generation and Initial Analysis of more than
 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
 2002, 99(26), 16899-16903"

ORIGIN

Query Match 81.0%; Score 17; DB 7; Length 638;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
 |||||

Db 458 GTGCTGTAGTGGCGGG 442
 |||||

RESULT 44

BW967847/c

LOCUS

DEFINITION BW967847 full-length enriched swine cDNA library, adult ovary Sus
 scrofa cDNA clone OVR010096F06 5', mRNA sequence.

ACCESSION

VERSION BW967847

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1 (bases 1 to 716)
 Unishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
 Okumura,N., Hamasima,N. and Awata,T.
 PEDE (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 14681463
 Contact: Hirohide Unishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences

2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627

Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.

FEATURES
 source

1..716 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="OVR010096F06"
 /tissue_type="ovary"
 /dev_stage="adult"
 /clone_lib="full-length enriched swine cDNA library, adult
 ovary"

ORIGIN

Query Match 81.0%; Score 17; DB 5; Length 716;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
 |||||

Db 594 GTGCTGTAGTGGCGGG 578
 |||||

RESULT 45

DN994620/c

LOCUS

DEFINITION DN994620 Human adult whole brain, large insert, pCMV expression
 library Homo sapiens cDNA clone TC116396 5' similar to Homo sapiens
 metal-regulatory transcription factor 1 (MTF1), mRNA sequence.

ACCESSION

VERSION DN994620.1 GI:66254451

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 722)

Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
 Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
 Zhang,X., Jay,G. and He,W.

High-throughput cloning of full-length human cDNAs directly from
 cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)

CONTACT: Kovacs, KF

High Throughput cDNA Cloning

Origene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 3188

Fax: 301 340 8606

Email: cDNA@origene.com

This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.

Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com

Seq primer: pCMV6 Sprieme forward vector primer, Origene
 Technologies Inc.

Location/Qualifiers

1..722

FEATURES
 source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC116396"
/tissue_type="Whole brain"
/clone_lib="Human adult whole brain, large insert, PCMV
expression library"
/note="Organ: Brain; Vector: pCMV6-XL5; Site 1: EcoRI;
Site 2: XhoI/SalI compatible end ligation; Oligo-dT primed
reverse transcription optimized for large and GC rich mRNA
transcripts, cDNA size selection, optimized ligation for
large inserts into mammalian expression vector, random
clones selected for end sequence verification of
full-length genes"

ORIGIN

Query Match 81.0%; Score 17; DB 8; Length 722;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGCGGGG 21
|||||

Db 565 GTGCTGTAGTGCGGGG 549
|||||

RESULT 46
AL702908/c
LOCUS
DEFINITION
AL702908 755 bp mRNA linear EST 04-SEP-2003
DKFZp686F0317_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686F0317 5', mRNA sequence.
ACCESSION
VERSION
AL702908.1 GI:19686263
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 755)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE
EST (Duesterhoeft, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686F0317) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686F0317"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 81.0%; Score 17; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGCGGGG 21
|||||

Db 600 GTGCTGTAGTGCGGGG 584
|||||

RESULT 47
BU500524/c
LOCUS
DEFINITION
BU500524 889 bp mRNA linear EST 12-SEP-2002
AGENCOURT_7860803 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:6109541
5', mRNA sequence.
ACCESSION
VERSION
BU500524.1 GI:22801559
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: NIMH/LOQ
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2355 row: j column: 06
High quality sequence start: 3
High quality sequence stop: 707.
Location/Qualifiers
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6109541"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 64"
/note="Vector: pOTB7a; Site 1: CeuI; Site 2: SceI; This
library is a size selection of NIH_MGC_35_ from 3.0-4.5
kb. Size selection done at the National Institute of
Mental Health, NIH. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 81.0%; Score 17; DB 5; Length 889;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGCGGGG 21
|||||

Db 571 GTGCTGTAGTGCGGGG 555
|||||

RESULT 48
BI257931/c
LOCUS
DEFINITION
BI257931 939 bp mRNA linear EST 17-JUL-2001
602970872F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5110505 5',
mRNA sequence.
ACCESSION
VERSION
BI257931.1 GI:14813786
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11267 row: o column: 18
 High quality sequence stop: 816.
 Location/Qualifiers
 1..939

FEATURES

source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5110505"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN

Query Match 81.0%; Score 17; DB 2; Length 939;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 92 GTGCTGTAGTGGCGGG 76

RESULT 49

BE796390/c

LOCUS BE796390 960 bp mRNA linear EST 20-SEP-2000
 DEFINITION 601592115F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946178 5', mRNA sequence.

ACCESSION BE796390

VERSION BE796390.1 GI:10217588

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

1 (bases 1 to 960)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCW805 row: n column: 03

High quality sequence stop: 706.

Location/Qualifiers

1..960

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3946178"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTS7; Site 1: XhoI; Site 2:

ORIGIN

Query Match 81.0%; Score 17; DB 2; Length 960;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 521 GTGCTGTAGTGGCGGG 505

RESULT 50

DQ052866/c

LOCUS DQ052866

DEFINITION Pan troglodytes MTF1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 1831 bp DNA linear GSS 02-JUN-2005

ACCESSION DQ052866

VERSION DQ052866.1 GI:66898813

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Pan.

REFERENCE 1 (bases 1 to 1831)

AUTHORS

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

(er) PLOS Biol. 3 (6), E170 (2005)

JOURNAL PUBMED

REFERENCE 2 (bases 1 to 1831)

AUTHORS

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

TITLE

JOURNAL

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES

Location/Qualifiers

1..1831

source

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1..>1831

/gene="MTF1"

/locus_tag="HCL13398"

ORIGIN

Query Match 81.0%; Score 17; DB 11; Length 1831;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 458 GTGCTGTAGTGGCGGG 442

Search completed: January 27, 2006, 07:06:35

Job time : 1560.5 secs

This page blank (uspo^{te})

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:38:14 ; Search time 1554.5 Seconds
(without alignments)
632.055 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21

Sequence: 1 cccgtgaggaactwctgtct.21

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gssi:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	85.7	197	2	BB245383 BB245383
2	18	85.7	290	1	BB091924 BB091924
3	18	85.7	310	1	BB042602 BB042602
C 4	18	85.7	653	5	BW844757 BW844757
C 5	17.8	84.8	403	7	CO858932 LM SL5 00
C 6	17.8	84.8	747	5	BU427835 BU427835
7	17.6	83.8	785	10	CE322782 tigr-gss-
8	17.6	83.8	858	5	BU214119 603756067
9	17.4	82.9	266	2	BB566123 BB566123
10	17.4	82.9	378	5	BQ55287 NKR0092
C 11	17.4	82.9	520	9	AZ622420 AZ622420
C 12	17.4	82.9	536	9	AZ373738 LM0156F01
13	17.4	82.9	559	1	AL773761 AL773761
14	17.4	82.9	582	10	CW879538 shs2kds38-
C 15	17.4	82.9	595	3	BJ100164 BJ100164
C 16	17.4	82.9	610	1	AL963378 AL963378
C 17	17.4	82.9	611	10	CE726956 tigr-gss-
C 18	17.4	82.9	629	10	CZ408044 1003747 R
19	17.4	82.9	642	1	AL864604 AL864604
20	17.4	82.9	683	6	CA845679 hab7zh11.
21	17.4	82.9	759	10	AG484074 Mus muscu
22	17.4	82.9	764	11	CR010258 Reverse s

AG545689 Mus muscu	784	10	AG545689
CR038774 Reverse s	825	11	CR038774
DN033350 JGI CAAR9	828	8	DN033350
DN074071 JGI_CABD8	854	8	DN074071
CX382809 JGI_XZT54	880	8	CX382809
BX751267 BX751267	886	5	BX751267
EX763496 BX763496	893	5	EX763496
BU01123 AGENCOURT	967	5	BU01123
CG58473 ZMMB8C026	1022	10	CG58473
CF223086 AGENCOURT	1177	6	CF223086
BU199108 DBCKC03	2319	5	BU199108
BB466847 BB466847	197	2	BB466847
BB287229 BB287229	262	2	BB287229
BB132524 BB132524	291	1	BB132524
BB256553 BB256553	319	2	BB256553
BB459406 BB459406	328	2	BB459406
BB470056 BB470056	333	2	BB470056
BB161894 BB161894	340	1	BB161894
CB766373 AMGNNUC:N	418	6	CB766373
AI848082 UI-M-AP1-	460	1	AI848082
DE020245 Branchios	501	11	DE020245
BM801116 BM801116	511	5	BM801116
CW315637 104_806_1	514	10	CW315637
DE024899 Branchios	542	11	DE024899
CO622122 DG9-226d2	546	7	CO622122
DN349087 LIB3578-0	546	8	DN349087
CAB83299 B0102D04-	547	6	CAB83299
AQ924133 RPCI-23-2	556	9	AQ924133
AZ251648 RPCI-23-9	606	9	AZ251648
CE688109 tigr-gss-	624	10	CE688109
CA775247 i086e11.x	671	6	CA775247
BB360213 BB360213	683	2	BB360213
CAB83022 B0100E12-	692	6	CAB83022
DN753682 GL-CF-104	713	8	DN753682
DN371296 LIB3733-0	742	8	DN371296
CR271570 Reverse s	749	11	CR271570
BM964299 UI-M-EQO-	757	3	BM964299
CB903274 ttrc033xk	757	6	CB903274
CR140120 Reverse s	761	11	CR140120
AG595402 Mus muscu	762	10	AG595402
AG497569 Mus muscu	763	10	AG497569
BH489544 BOHJ063TF	773	9	BH489544
CV104092 AGENCOURT	794	7	CV104092
CR187048 Reverse s	808	11	CR187048
CD613178 56024846H	835	6	CD613178
CR228728 Forward s	929	11	CR228728
BQ712870 AGENCOURT	970	5	BQ712870
BG294134 602391203	1294	8	BG294134
DN714254 CNB101-F0	1439	8	DN714254
AK047798 Mus muscu	1585	4	AK047798
BG207001 RST26465	284	2	BG207001
BG190545 RST9617 A	381	2	BG190545
AQ927438 RPCI-23-2	422	9	AQ927438
CL266734 Ggal 124d	472	10	CL266734
BY728984 BY728984	656	5	BY728984
CK175061 EST764381	817	7	CK175061
CK175062 EST764382	842	7	CK175062
AKW59677 46520 MAR	394	1	AKW59677
CF625924 zmrw05_0	606	6	CF625924
CF627144 zmrw05_0	606	6	CF627144
CA348469 679797 NC	647	6	CA348469
BZ313443 h207d10.b	690	9	BZ313443
BZ320336 h207d10.g	710	9	BZ320336
BZ97088 PUGG2221D	748	9	BZ97088
CC972986 PUGG101TD	753	9	CC972986
CC020942 EST817035	956	7	CC020942
CG698568 ZMMB8C011	958	10	CG698568
CL988880 ZMMB8E000	1070	10	CL988880
CE376730 tigr-gss-	208	10	CE376730
BB590797 BB590797	228	2	BB590797
AW445570 B1852 MAR	232	1	AW445570
BB581243 BB581243	242	2	BB581243

96 16.4 78.1 248 2 BB452304 BB452304
 c 97 16.4 78.1 277 2 BB485218 BB485218
 c 98 16.4 78.1 306 10 CG473023 CG473023 OST316 Mu
 c 99 16.4 78.1 307 2 BB395457 BB395457
 c 100 16.4 78.1 319 1 BB130137 BB130137

ALIGNMENTS

RESULT 1
 BB245383 197 bp mRNA linear EST 06-JUL-2000
 LOCUS BB245383 RIKEN full-length enriched, 7 days neonate cerebellum Mus
 DEFINITION musculus cDNA clone A73009B02 3', mRNA sequence.

ACCESSION
 VERSION BB245383.1 GI:8938129

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
 AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sugabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE

JOURNAL

COMMENT

RIKEN Mouse ESTs (Konno,H., et al.)
 Unpublished (2000)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermotabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp/>) for
 further details.

FEATURES

source

Location/Qualifiers

1..197
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A73009B02"
 /tissue type="cerebellum"
 /dev stage="7 days neonate"
 /lab host="DH10B"
 /clone lib="RIKEN full-length enriched, 7 days neonate
 cerebellum"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATTCGAGTTAATAATATCCGCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 85.7%; Score 18; DB 2; Length 197;
 Best Local Similarity 90.0%; Pred. No. 5.le+02;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTTCTGTC 20

Db 127 CCTGTGAGGAACTAGTGC 146

RESULT 2

BB091924

LOCUS

DEFINITION

BB091924 RIKEN full-length enriched, 12 days embryo, embryonic body
 between diaphragm region and neck Mus musculus cDNA clone
 9430032C22 3', mRNA sequence.

ACCESSION

VERSION BB091924.1 GI:8675171

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 290)
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sugabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermotabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,

Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

Location/Qualifiers
1..290
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9430032C22"
/tissue_type="embryonic body between diaphragm region and
neck"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo,
embryonic body between diaphragm region and neck"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAATAATTAATCCCTCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI."

ORIGIN

Query Match 85.7%; Score 18; DB 1; Length 290;
Best Local Similarity 90.0%; Pred. No. 5.5e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTC 20

DB 219 CCCTGTGAGGAAGTCTGTC 238

RESULT 3

BB042602 310 bp mRNA linear EST 23-JUN-2000
LOCUS BB042602 RIKEN full-length enriched, 13 days embryo male testis Mus
musculus cDNA clone 6030464H05 3', mRNA sequence.

BB042602

BB042602.1 GI:8448988

EST.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
Hayashizaki, Y.

TITLE JOURNAL COMMENT

RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitasuna, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

Location/Qualifiers
1..310
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="6030464H05"
/sex="male"
/tissue_type="testis"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 13 days embryo
male testis"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 5.0 and subtraction to Rot = 100.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTTAATAATTAATCCCTCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN

Query Match 85.7%; Score 18; DB 1; Length 310;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;

Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTC 20

|||||

DB 242 CCCTGTGAGGAAGTCTGTC 261

RESULT 4

LOCUS BW844757/c

DEFINITION

BW844757 653 bp mRNA linear EST 23-MAY-2005
Amphioxus Branchiostoma floridae unpublished cDNA library,
neural whole animal Branchiostoma floridae cDNA clone bne023019
5', mRNA sequence.

ACCESSION

BW844757

```

VERSION      BW844757.1  GI:66452973
KEYWORDS
SOURCE       Branchiostoma floridae (Florida lancelet)
ORGANISM     Branchiostoma floridae
             Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
             Branchiostoma.
REFERENCE    1 (bases 1 to 653)
AUTHORS      Yu, J., Holland, L.Z., Shin-i, T., Kohara, Y., Satou, Y. and Satoh, N.
TITLE        Expressed genes in Branchiostoma floridae
JOURNAL      Unpublished (2005)
COMMENT      Contact: Tadasu Shin-i
             Center For Genetic Resource Information
             National Institute of Genetics
             1111 Yata, Mishima, Shizuoka 411-8540, Japan
             Tel: 81-559-81-6856
             Fax: 81-559-81-6855
             Email: tshini@genes.nig.ac.jp.
FEATURES     Location/Qualifiers
             1..653
             /organism="Branchiostoma floridae"
             /mol_type="mRNA"
             /db_xref="taxon:7739"
             /clone="bbs023o19"
             /tissue_type="whole animal"
             /dev_stage="neurula"
             /clone_lib="Amphioxus Branchiostoma floridae unpublished
             cDNA library, neurula whole animal"
ORIGIN
Query Match      85.7%; Score 18; DB 5; Length 653;
Best Local Similarity 90.0%; Pred. No. 6.4e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCTGTGAGGAACCTGCTGT 21
Db      188 CCTGTGAGGACCACTGTCT 169

RESULT 5
LOCUS     CO858932/c
DEFINITION
LOCUS     CO858932
VERSION   CO858932.1  GI:55918739
KEYWORDS  EST.
SOURCE    Locusta migratoria (migratory locust)
ORGANISM  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Oedipodinae; Locusta.
REFERENCE 1 (bases 1 to 403)
AUTHORS    Kang, L., Chen, X., Zhou, Y., Liu, B., Zheng, W., Li, R., Wang, J. and
             Yu, J.
TITLE      The analysis of large-scale gene expression correlated to the phase
             changes of the migratory locust
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 101 (51), 17611-17615 (2004)
PUBMED    15591108
COMMENT    Contact: Le Kang
             National Laboratory of Integrated Management of Insect Pests and
             Rodents
             Institute of zoology, Chinese Academy of Sciences
             25 Beisihuanxi Road, Haidian, Beijing, 100080, China
             Tel: 86-10-68597439
             Fax: 86-10-68597486
             Email: lkang@panda.iaz.ac.cn
             High quality sequence stop: 403.
FEATURES     Location/Qualifiers
             1..403
             /organism="Locusta migratoria"
             /mol_type="mRNA"
             /db_xref="taxon:7004"
             /tissue_type="hind-legs"

/dev_stage="fifth-instar"
/clone_lib="Locusta migratoria solitary phase's hind-legs cDNA library"
hind-legs cDNA library"

Query Match      84.8%; Score 17.8; DB 7; Length 403;
Best Local Similarity 90.5%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCTGTGAGGAACCTGCTGTCT 21
Db      62 CCTGTGAGGCACTGCTGTCT 42

RESULT 6
LOCUS     BU427835
DEFINITION
LOCUS     BU427835
VERSION   BU427835.1  GI:25920511
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
             Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 747)
AUTHORS    Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
             Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE      A Comprehensive Collection of Chicken cDNAs
JOURNAL    Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED    12445392
COMMENT    Contact: Simon Hubbard
             Department of Biomolecular Sciences
             University of Manchester Institute of Science and Technology
             (UMIST)
             PO Box 88, Manchester, M60 1QD, UK
             Tel: 01612008930
             Fax: 01612360409
             Email: Simon.Hubbard@umist.ac.uk.
FEATURES     Location/Qualifiers
             1..747
             /organism="Gallus gallus"
             /mol_type="mRNA"
             /strain="Layer and broiler"
             /db_xref="taxon:9031"
             /clone="CHEST228b23"
             /sex="Male and female"
             /tissue_type="Chondrocytes isolated from growth plate
             cartilage"
             /dev_stage="adult"
             /lab_host="DH10B"
             /clone_lib="CSEQRBN09"
             /notes="Vector: pBluescript II KS(+); Site 1: EcoRI;
             Site 2: NotI; this normalized library was constructed from
             1 million independent clones. cDNA synthesis was initiated
             using an oligo(dT) primer, using methylated C in the first
             strand synthesis reaction. Following this first strand
             reaction, double-stranded cDNA was blunted, ligated to
             NotI adapters, digested with EcoRI, size-selected, and
             cloned into the NotI and EcoRI compatible sites of a
             custom modified MCS of the pBluescript (KS+) vector. The
             library was normalized in 2 rounds using conditions
             adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
             Bonaldo et al., Genome Research 6 (1996): 791, except that
             a significantly longer reannealing hybridization was
             used."

Query Match      84.8%; Score 17.8; DB 5; Length 747;
Best Local Similarity 90.5%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 CCTGTGAGGAAGTCTGTCT 21
DB 425 CCTGTGAGGAGCTGTCTCT 445

RESULT 7
CE322782
LOCUS tigr-gss-dog-17000361363031 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE322782
VERSION CE322782.1 GI:361311132
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE
AUTHORS 1 (bases 1 to 785)
 Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers
 1..785
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 83.8%; Score 17.6; DB 10; Length 785;
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGTGAGGAAGTCTGTCT 21
DB 501 TGTGAGGAAGTCTGTCT 518

RESULT 8
BU214119
LOCUS BU214119.1 GI:25389868
DEFINITION 603756067F1 CSEQCHN04 Gallus gallus cdna clone ChEST667e17 5', mRNA
 sequence.
ACCESSION BU214119
VERSION BU214119.1 GI:25389868
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE
AUTHORS 1 (bases 1 to 858)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..858
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hixex"
 /db_xref="taxon:9031"
 /clone="ChEST667e17"
 /tissue_type="whole embryo"
 /dev_stage="20-21"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN04"
 /note="Organ: whole embryo; Vector: pBluescript II KS(+);
 Site 1: EcoRI; Site 2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN
 Query Match 83.8%; Score 17.6; DB 5; Length 858;
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTGTGAGGAAGTCTGTCT 20
DB 775 CTGTGAGGAAGTCTGTCT 792

RESULT 9
BB566123
LOCUS BB566123 RIKEN full-length enriched, 13 days embryo liver Mus
DEFINITION musculus cdna clone 250002A19 5', mRNA sequence.
ACCESSION BB566123
VERSION BB566123.1 GI:11457015
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 266)
 Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.,
 Carninci,P., Hanagaki,T., Hayatsu,N., Hirooka,T., Hirozane,T.,
 Hodoiyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J.,
 Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A.,
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y.,
 Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K.,
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
 Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T.,
 Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A.,
 Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax.: 81-45-503-9216

Fax: 81-43-503-9248
 Email: genome-rc@esc.riken.jp, URL: <http://genome.esc.riken.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermotabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. *Genome Res.* 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp/>) for
 further details.

FEATURES

```

1..266
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/cln="2500002A19"
/tissue_type="liver"
/dev_stage="13 days embryo"
/lab_host="SOUR"
/clone_lib="RIKEN full-length enriched, 13 days embryo
liver"
/note="Site 1: XhoI; Site 2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGGATCAAGAGCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATTTCGATTAAATAAATATACCCCCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and SstI."

```

ORIGIN

```
Query Match      82.9%; Score 17.4; DB 2; Length 266;
Best Local Similarity 85.7%; Pred. NO. 1.1e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CCCTGTGAGGAACCTWCTGCT 21
|||
Db 121 CCCTGTGTGGAACCTACGGTCT 141

RESULT 10
BQ655287 378 bp mRNA linear EST 07-MAY-2003
LOCUS NRKV092.E02.F NRKV (Nsf Xylem Root wood Vertical) Pinus taeda CDNA
DEFINITION clone NRKV092.E02.5, similar to Arabidopsis thaliana sequence
AT-5G09810 ACTIN 2/7 (sp|P53492) see
http://mings.csf.defnroji.thal/db/index.html. mRNA sequence.

ACCESSION BQ655287
VERSION BQ655287.1 GI:21787613
KEYWORDS EST.

KEYWORDS	SOURCE	ORGANISM
ESL.	Pinus taeda (loblolly pine)	Pinus taeda
		Pinus taeda

UKRAINIAN
 Fungus caedua
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 378)
 Sederoff, R.
 Molecular Basis of Wood Formation in the Pine Megagenome
 TITLE

JOURNAL
COMMENT

Unpublished (2000)
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu, jerrl.johnson@ncsu.edu
please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further
information.

Seq primer: T3.

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10
11. Feature 11	Source 11
12. Feature 12	Source 12
13. Feature 13	Source 13
14. Feature 14	Source 14
15. Feature 15	Source 15
16. Feature 16	Source 16
17. Feature 17	Source 17
18. Feature 18	Source 18
19. Feature 19	Source 19
20. Feature 20	Source 20
21. Feature 21	Source 21
22. Feature 22	Source 22
23. Feature 23	Source 23
24. Feature 24	Source 24
25. Feature 25	Source 25
26. Feature 26	Source 26
27. Feature 27	Source 27
28. Feature 28	Source 28
29. Feature 29	Source 29
30. Feature 30	Source 30
31. Feature 31	Source 31
32. Feature 32	Source 32
33. Feature 33	Source 33
34. Feature 34	Source 34
35. Feature 35	Source 35
36. Feature 36	Source 36
37. Feature 37	Source 37
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40. Feature 40	Source 40
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80. Feature 80	Source 80
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88. Feature 88	Source 88
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90. Feature 90	Source 90
91. Feature 91	Source 91
92. Feature 92	Source 92
93. Feature 93	Source 93
94. Feature 94	Source 94
95. Feature 95	Source 95
96. Feature 96	Source 96
97. Feature 97	Source 97
98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

FEATURES

```

1. .378
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXRV092_E02"
/tissue_type="Xylem"
/cell_type="Root (Primary)"
/dev_stage="Transitional"
/lab_host="X11-Blue"
/clone_lib="NXRV Root wood Vertical"
/notes="vector: pluscript SK; Sitel: sco RI; Site_2: xhoI; The library is from primary xylem scraped from the roots of a twelve year old tree in the transitional phase from juvenile wood to mature wood production. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTGGCGACGAC'."

```

ORIGIN

Query Match	82.9%;	Score 17.4;	DB 5;	Length 378;
Best Local Similarity	85.7%;	Pred. No. 1.2e+03;		
Matches 18: Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 CCCTGTGAGGAACCTWCCTGTCT 21
|||
db 317 CCCTGTGAGGAACCTCAGTGT 33
|||

RESULT 11	
AZ622420/c	
LOCUS	DEFINITION

AZ6222420 520 bp DNA linear GSS 13-DEC-2000
 1M0459C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0459C13 F. genomic survey sequence.

ACCESSION	AZ622420	
VERSION	AZ622420.1	GI:11744610
KEYWORDS	GSS.	

REPRODUCED	SOURCE
CCS:	<i>Mus musculus</i> (house mouse)

SOURCE	ORGANISM
Mus musculus (house mouse)	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurornathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, N., Stokes, R., Tingey, A., von Niederhausern A. and Wright, D. Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kbp
plasmid inserts

plasmid inserts
Unpublished (2000)

JOURNAL
UNPUBLISHED (2000)
CONTACT: Robert B Weiss
COMMENT

CONTACT: ROBERT B. WEISS
University of Utah Genome Center

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Tel: 801 585 7177
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0459 row: C column: 13

Seq primer: CCGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 520.

FEATURES

source

1. 520
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0459C13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 520;

Best Local Similarity 85.7%; Pred. No. 1.2e+03; Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCCTGTGAGGAAGTCTGTCT 21

Db 494 CCCTGTGAGGAAGTCTGTCT 474

RESULT 12

AZ373738

LOCUS

DEFINITION AZ373738 536 bp DNA linear GSS 02-OCT-2000
 clone UUGC1M0126F01 F, Genomic survey sequence.

ACCESSION

AZ373738

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Scuriongnathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 536)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0126 row: F column: 01

Seq primer: CCGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 536.

FEATURES

source

1. 536
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0126F01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 536;

Best Local Similarity 85.7%; Pred. No. 1.2e+03; Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCCTGTGAGGAAGTCTGTCT 21

Db 493 CCCTGTGAGGAAGTCTGTCT 513

RESULT 13

AL773761

LOCUS

DEFINITION AL773761 XGC-gastrula Xenopus tropicalis cDNA clone Tgas071p03 5',
 mRNA sequence.

ACCESSION

AL773761

VERSION

EST.

KEYWORDS

Xenopus tropicalis (western clawed frog)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 559)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2001 (11_2003)

Unpublished (2003)

On Jun 25, 2002 this sequence version replaced gi:21559465.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: tropesanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13

gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with

EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site1: EcoRI; Site2: NotI

Host: Escherichia coli XL1-blue

```

Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas071p03.plcSP6
Sequencing primer: SP6.
FEATURES
    source
        1..559
            /organism="Xenopus tropicalis"
            /mol_type="mRNA"
            /db_xref="taxon:8364"
            /clone="TGas071p03"
            /dev_stage="gastrula (stages 10.5-12 mixed)"
            /lab_host="Escherichia coli XL1-blue"
            /clone_lib="XGC-gastrula"
            /notes="vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
ORIGIN
Query Match      82.9%;   Score 17.4;   DB 1;   Length 559;
Best Local Similarity 85.7%;   Pred. No. 1.3e+03;
Matches 18;   Conservative 1;   Mismatches 2;   Indels 0;   Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||||:|||||
Db 246 CCATGTGAGGAAGTACTGACT 266

RESULT 14
CW879538
LOCUS
DEFINITION
    CW879538 582 bp DNA linear GSS 12-FEB-2005
    sbs2kd38-90.b_094.ab1 Whole-genome shotgun library of the elephant
    shark (aka elephant fish) Callorhynchus milii genomic, genomic
    survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    CW879538.1 GI:59706173
    Callorhynchus milii (elephantfish)
    Callorhynchus milii
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
    Holocephali; Chimaeriformes; Callorhynchidae; Callorhynchus.
REFERENCE
    1 (bases 1 to 582)
    Venkatesh,B., Tay,A., Dandona,N., Patil,J.G. and Brenner,S.
    A compact cartilaginous fish model genome
    Curr. Biol. 15 (3), R82-R83 (2005)
JOURNAL
PUBMED
    15694293
COMMENT
    Contact: Venkatesh B
    Molecular Genetics Lab
    Institute of Molecular and Cell Biology
    61 Biopolis Drive, Singapore 138673
    Tel: 65 6586 9571
    Fax: 65 6779 1117
    Email: mcbbv@imcb.a-star.edu.sg
    Whole-genome shotgun sequences of the elephant shark (aka elephant
    fish)
    Class: shotgun.
FEATURES
    source
        1..582
            /organism="Callorhynchus milii"
            /mol_type="genomic DNA"
            /db_xref="taxon:7868"
            /sex="Male"
            /tissue_type="Testis"
            /clone_lib="Whole-genome shotgun library of the elephant
            shark (aka elephant fish)"
ORIGIN
Query Match      82.9%;   Score 17.4;   DB 10;   Length 582;
Best Local Similarity 85.7%;   Pred. No. 1.3e+03;
Matches 18;   Conservative 1;   Mismatches 2;   Indels 0;   Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||||:|||||

```

Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS SEQUENCE ID: TGae133g15.plkSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13
 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli XL1-blue.

FEATURES

source

Location/Qualifiers
 1..610
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TGae133g15"
 /dev_stage="gastrula (stages 10.5-12 mixed)"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-gastrula"
 /notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from stages
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
 into pCS107 with EcoRI at the 5' end and NotI at the 3'
 end."

ORIGIN

Query Match 82.9%; Score 17.4; DB 1; Length 610;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGTGAGGAAGTCTGTCT 21
 |||||||||
 Db 161 CCATGTGTGAGGAAGTCTGACT 181

RESULT 17

CE726956/c

LOCUS

DEFINITION 611 bp DNA linear GSS 30-SEP-2003
 tigr-gss-dog-17000315262749 Dog Library Canis familiaris genomic,
 genomic survey sequence.

CE726956

GSS.

CE726956.1 GI:37067076

SOURCE

Canis familiaris (dog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE

AUTHORS

1 (bases 1 to 611)
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)

PUBMED

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

source

Location/Qualifiers
 1..611
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 82.9%; Score 17.4; DB 10; Length 611;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGTGAGGAAGTCTGTCT 21

Db 173 CCTGTGTGAGGAAGTCTGTCT 153

RESULT 18

CZ408044

LOCUS

DEFINITION 629 bp DNA linear GSS 06-APR-2005
 1003747 RP42 Bos taurus genomic clone RP42-14N03, genomic survey
 sequence.

ACCESSION CZ408044

VERSION CZ408044.1

KEYWORDS GI:62294882

SOURCE GSS.

ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 629)
 Sonstegard, T.S., Van Tassel, C.P., Capuco, A.V., de Jong, P.,
 Matukumalli, L.K., Shade, L.S., Bosak, S., Rubenfield, M. and
 Gaebler, L.C.

TITLE

JOURNAL

COMMENT

Bovine BAC End Sequences from Library RPCI-42
 Unpublished (2005)
 Contact: Tad S. Sonstegard
 Bovine Functional Genomics Laboratory
 Animal and Natural Resources Institute
 Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
 Tel: 3015048416
 Fax: 3015048414

Email: tads@anri.barc.usda.gov

Clones are derived from the bovine BAC library RPCI-42
 (http://bacpac.choi.org/mbovine42.htm). For BAC library
 availability, please contact Pieter de Jong (pjejong@mail.choi.org).
 Clones may be purchased from BACPAC Resources
 (http://www.choi.org/bacpac/ordering_information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by USDA-ARS-BFGL.

Plate: 14 row: N column: 03

Seq primer: CTGGCCGTCGACATTAGG

Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..629
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="RP42-14N03"
 /sex="male"
 /cell_type="Blood"
 /clone_lib="RP42"
 /note="Vector: pBACe3.6; Site 1: MboI; Site 2: MboI;
 RPCI-42 Bovine BAC library (Maie Holstein) produced by
 Pieter de Jong"

ORIGIN

Query Match 82.9%; Score 17.4; DB 10; Length 629;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGTGAGGAAGTCTGTCT 21

Db 462 CACTGTGTGAGGTACTACTGTCT 482

RESULT 19

AL864604


```

COMMENT
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source
Location/Qualifiers
1..759
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-379H12.T7"
/sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 82.9%; Score 17.4; DB 10; Length 759;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
||||| ||||| ||||| ||||| |||||
DB 520 CCTGAGAGCAACTTCTGTCT 540

RESULT 22
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPP360c24, genomic survey sequence.
CR010258
VERSION 1 GI:49743249
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
source
Location/Qualifiers
1..764
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP360c24"
/clone_lib="MHPP"

ORIGIN
Query Match 82.9%; Score 17.4; DB 11; Length 764;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
||||| ||||| ||||| ||||| |||||
DB 663 CCTGAGAGCAACTTCTGTCT 683

RESULT 23
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPP129i23, genomic survey sequence.
CR038774
VERSION 1 GI:49771829
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
15574823
2 (bases 1 to 784)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..784
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-460E18.TJ"
/sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 82.9%; Score 17.4; DB 10; Length 784;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
||||| ||||| ||||| ||||| |||||
DB 403 CCTGAGAGCAACTTCTGTCT 383

RESULT 24
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPP129i23, genomic survey sequence.
CR038774
VERSION 1 GI:49771829
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 825)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J., and Bradley,A.

TITLE

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES

source

1..825
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPPI29123"
/clone_lib="MHPp"

ORIGIN

Query Match 82.9%; Score 17.4; DB 11; Length 825;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGCAACTWCTGTCT 21

Db 661 CCCTGAGCAACTTCTGTCT 681

RESULT 25

DN033350

LOCUS

DEFINITION
JGI_CAAR9837.fwd NIH_XGC_tropliv1 Xenopus tropicalis cDNA clone
IMAGE:7741910 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE

AUTHORS

Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.

DOE Joint Genome Institute Xenopus tropicalis EST project

Unpublished (2004)

TITLE

JOURNAL

COMMENT

Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710

Email: cdna@jgi-psf.org

Tissue Procurement: Robert M. Grainger

cDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of
the JGI Clone ID and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.

Plate: CAAR 0101 row: i column: 12

High quality sequence stop: 785.

Location/Qualifiers

1..828

source

/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7741910"
/sex="male"

/tissue_type="Liver"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage resistant cells"
/clone_lib="NIH_XGC_tropliv1"
/note="Vector: PCS107; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from 5 ug of poly A+ RNA by oligo-dT
priming

(5'-GAGAGAGAGAGAGAGACTAGTCTCGAGTTTTTTTTTTTTTTT-3')
and Stratascript reverse transcriptase. After ligation of
EcoRI adapters (5'-AATTCGACGAGG-3') followed by kinasing
adapters and by XhoI digestion, the cDNA was size selected
by chromatography on Sepharose CL-2B columns and fractions
containing cDNAs larger than 1000 bp were ligated into
EcoRI/XhoI-digested PCS107. Reference for library
construction: Current Genomics 4, 635-644. Library
constructed by Michelle Tabb and Bruce Blumberg (Dept of
Developmental and Cell Biology, University of California,
Irvine)."

ORIGIN

Query Match 82.9%; Score 17.4; DB 8; Length 828;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGCAACTWCTGTCT 21

Db 307 CCATGTGAGCAACTACTGACT 327

RESULT 26

DN074071/c

LOCUS

DEFINITION
JGI_CAAR8095.rev NIH_XGC_troplun1 Xenopus tropicalis cDNA clone
IMAGE:7813425 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE

AUTHORS

Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.

DOE Joint Genome Institute Xenopus tropicalis EST project

Unpublished (2004)

TITLE

JOURNAL

COMMENT

Contact: Lindquist,E.A., Richardson,P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 5600

Fax: 925 296 5710

Email: cdna@jgi-psf.org

Tissue Procurement: Robert M. Grainger

cDNA Library Preparation: Bruce Blumberg Laboratory, University of

California, Irvine

DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.E. Consortium/LLNL:

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of
the JGI Clone ID and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.

Plate: CABD 0085 row: m column: 7

High quality sequence stop: 805.

Location/Qualifiers

1..854

source

/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7813425"

source

```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMBBc0267E13"
/lab_host="E. coli DH10B"
/clone_lib="ZMBBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match      82.9%; Score 17.4; DB 10; Length 1022;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||||:|||||
Db 868 CCGTGTGAGGAAGTCTGTCT 888

RESULT 32
CF223086
LOCUS
DEFINITION
AGENCOURT 15068014 NICHD XGC Emb7 Xenopus tropicalis cDNA clone
CF223086
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1177)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMW14629 row: n column: 04
High quality sequence start: 176
High quality sequence stop: 562.

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/clone="IMAGE:6976517"
/tissue_type="tailbud"
/dev_stage="embryo, stages 20-27"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Emb7"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match      82.9%; Score 17.4; DB 6; Length 1177;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 305 CCATGTGAGGAAGTCTGTCT 325

RESULT 33
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LOCUS
DEFINITION
DCBCKC03 DCB Homo sapiens cDNA, mRNA sequence.
BUI199108
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2319)
Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,
Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Cheng, Z. and Han, Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
Location/Qualifiers
1..2319
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Query Match      82.9%; Score 17.4; DB 5; Length 2319;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 2309 CCGTGTGCGGACCTACTGTCT 2289

RESULT 34
B4466847
LOCUS
DEFINITION
B4466847 RIKEN full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D230011A04 3', mRNA sequence.
B4466847
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 197)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A.,

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Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

source

1. .197
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="D230011A04"
/tissue_type="eyeball"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo
eyeball"
/notes="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTCGAGTTAATTAATTAATCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 81.0%; Score 17; DB 2; Length 197;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTGCTGT 19
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Db 126 CCCTGTGAGGAACCTGCTGT 144
|||||

RESULT 35
BB287229 262 bp mRNA linear EST 09-JUL-2000
LOCUS BB287229 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
DEFINITION Clone B020017L13 3', mRNA sequence.
ACCESSION BB287229
VERSION BB287229.1 GI:8987678

KEYWORDS

SOURCE ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 262)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .262
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="B020017L13"
/tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
/notes="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTCGAGTTAATTAATTAATCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match

81.0%; Score 17; DB 2; Length 262;

Best Local Similarity 89.5%; Pred. No. 1.7e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGTGAGGAAGTCTGTC 20
 Db 196 CCTGTGAGGAAGTCTGTC 214
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RESULT 36
 BB132524
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BB132524 291 bp mRNA linear EST 28-JUN-2000
 BB132524 RIKEN full-length enriched, adult male bone Mus musculus
 cDNA clone 983000ID09 3', mRNA sequence.
 BB132524
 BB132524.1 GI:8786914
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 291)

REFERENCE
 AUTHORS
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
 Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
 Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
 Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
 Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
 Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
 Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
 Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
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 Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
 Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
 Hayashizaki,Y.
 RIKEN Mouse ESTs (Konno,H., et al.)
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 Contact: Yoshihide Hayashizaki
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 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
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 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S.,
 Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermotabilization and thermoactivation of thermostable enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
 Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 source
 Location/Qualifiers
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 /organism="Mus musculus"
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 /db_xref="taxon:10090"
 /clone="983000ID09"
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 /clone_lib="RIKEN full-length enriched, adult male bone"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 195.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATCTCGAGTTAATTAATTCCTCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pluescript KS(+) after bulk excision from Lambda
 PLC I."

ORIGIN

Query Match 81.0%; Score 17; DB 1; Length 291;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGTGAGGAAGTCTGTC 20
 Db 225 CCTGTGAGGAAGTCTGTC 243
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RESULT 37
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BB256553 319 bp mRNA linear EST 06-JUL-2000
 BB256553 RIKEN full-length enriched, 7 days neonate cerebellum Mus
 musculus cDNA clone A730074C15 3', mRNA sequence.
 BB256553
 BB256553.1 GI:8949386
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 319)

REFERENCE
 AUTHORS
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
 Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
 Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
 Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
 Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
 Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
 Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
 Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
 Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
 Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
 Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
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 The Institute of Physical and Chemical Research (RIKEN)
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 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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 Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
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FEATURES
 source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="983000ID09"
 /sex="male"
 /tissue_type="bone"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, adult male bone"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia

Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.		Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.	
FEATURES		FEATURES	
source		source	
Location/Qualifiers		Location/Qualifiers	
1. .319 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="A730074C15" /tissue_type="cerebellum" /dev_stage="7 days neonate" /lab_host="DH10B" /clone_lib="RIKEN full-length enriched, 7 days neonate cerebellum" /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATAATTAATCCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."		1. .328 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="D130061E08" /tissue_type="spinal ganglion" /dev_stage="12 days embryo" /lab_host="DH10B" /clone_lib="RIKEN full-length enriched, 12 days embryo spinal ganglion" /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCAACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATAATTAATCCCTCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."	
ORIGIN		ORIGIN	
Query Match 81.0%; Score 17; DB 2; Length 319; Best Local Similarity 89.5%; Pred. No. 1.8e+03; Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		Query Match 81.0%; Score 17; DB 2; Length 328; Best Local Similarity 89.5%; Pred. No. 1.8e+03; Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 CCCTGTGAGGAAGTCTGCTGT 19	Qy	1 CCCTGTGAGGAAGTCTGCTGT 19
Db	252 CCCTGTGAGGAAGTCTGCTGT 270	Db	262 CCCTGTGAGGAAGTCTGCTGT 280
RESULT 38		RESULT 39	
BB459406		BB470056	
LOCUS		LOCUS	
BB459406 RIKEN full-length enriched, 12 days embryo spinal ganglion		BB470056 RIKEN full-length enriched, 12 days embryo eyeball Mus	
Mus musculus cDNA clone D130061E08 3', mRNA sequence.		musculus cDNA clone D230030L20 3', mRNA sequence.	
ACCESSION		ACCESSION	
BB459406.1 GI:9354899		BB470056.1 GI:9387245	
VERSION		VERSION	
EST.		EST.	
Mus musculus (house mouse)		Mus musculus (house mouse)	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Konno,H., et al.) Unpublished (2000)		333 bp mRNA linear EST. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.	
TITLE		TITLE	
JOURNAL		JOURNAL	

REFERENCE	1 (bases 1 to 333)	266 CCCTGTGAGGAACTAGTGT 284
AUTHORS	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Iohi,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	BB161894 340 bp mRNA linear EST 29-JUN-2000 BB161894 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone A130064A09 3', mRNA sequence. BB161894 BB161894.1 GI:8817834 EST Mus musculus (house mouse) Mus musculus
TITLE	RIKEN Mouse ESTs (Konno,H., et al.)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
JOURNAL	Unpublished (2000)	1 (bases 1 to 340)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.	BB161894 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone A130064A09 3', mRNA sequence. BB161894 BB161894.1 GI:8817834 EST Mus musculus (house mouse) Mus musculus
FEATURES	Location/Qualifiers	Location/Qualifiers
source	1..333	1..340
	/organism="Mus musculus"	/organism="Mus musculus"
	/mol_type="mRNA"	/mol_type="mRNA"
	/db_xref="taxon:10090"	/db_xref="taxon:10090"
	/clone="D230030L20"	/clone="A130064A09"
	/tissue_type="eyeball"	/tissue_type="thymus"
	/dev_stage="12 days embryo"	/dev_stage="16 days neonate"
	/lab_host="DH10B"	/lab_host="DH10B"
	/clone_lib="RIKEN full-length enriched, 12 days embryo eyeball"	/clone_lib="RIKEN full-length enriched, 16 days neonate thymus"
	/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]. GAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5]. GAGAGAGATTCGAGTTAATTAATATCCCCCCCCCC 3'. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."	/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
ORIGIN		
Query Match	81.0%; Score 17; DB 2; Length 333;	
Best Local Similarity	89.5%; Pred. No. 1.8e+03;	
Matches	17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 CCCTGTGAGGAACTAGTGT 19 	

GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I."

ORIGIN

Query Match 81.0%; Score 17; DB 1; Length 340;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 19

|||||
Db 270 CCTGTGAGGAAGTCTGCT 288

RESULT 41

CB766373/c 418 bp mRNA linear EST 16-MAY-2003
LOCUS AMGNNUC:NRPI4-00056-G12-A W Rat pituitary (10472) Rattus norvegicus
DEFINITION cDNA clone nrpi4-00056-g12 5', mRNA sequence.

ACCESSION CB766373

VERSION CB766373.1 GI:29854764

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 418)

Angen EST Program.

Angen Rat EST Program

Unpublished (2003)

Contact: Dan Fitzpatrick

Angen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00056 row: g column: 12.

FEATURES

source

1..418

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone_lib="nrpi4-00056-g12"

/clone_lib="W Rat pituitary (10472)"

/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat pituitary adult female Wistar rat avg insert size 2.1 kb"

ORIGIN

Query Match 81.0%; Score 17; DB 6; Length 418;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTGTGAGGAAGTCTGCT 21

|||||
Db 362 CTGTGAGGAAGTCTGCT 344

RESULT 42

AI848082/c 460 bp mRNA linear EST 15-JUL-1999
LOCUS UI-M-AP1-agk-b-12-0-UI.s1 NIH BMAP_MST_N Mus musculus cDNA clone
DEFINITION UI-M-AP1-agk-b-12-0-UI 3', mRNA sequence.

ACCESSION AI848082

VERSION AI848082.1 GI:5491988

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

TITLES

AUTHORS

JOURNAL

PUBMED

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 460)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

8889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mst@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

1..460

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-AP1-agk-b-12-0-UI"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH BMAP_MST_N"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP MST_N library is a normalized library constructed from mouse striatum. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track.

The library was constructed as described by Bonaldo,

Lennon and Soares, Genome Research 6: 791-806, 1996.

Tissue provided by Ms. Annie Novakovich, Zivic-Miller

Laboratories.

TAG_TISSUE=corpus-striatum

TAG_LIB=NIH_BMAP_MST_N

TAG_SEQ=ACGGC"

ORIGIN

Query Match 81.0%; Score 17; DB 1; Length 460;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTGTGAGGAAGTCTGCT 21

|||||
Db 310 CTGTGAGGAAGTCTGCT 292

RESULT 43

DE020245 501 bp DNA linear GSS 06-APR-2005
LOCUS Branchiostoma floridae DNA, clone: CH302-032P18.R, genomic survey
DEFINITION sequence.

ACCESSION DE020245

VERSION DE020245.1 GI:62263715

KEYWORDS GSS.

SOURCE Branchiostoma floridae (Florida lancelet)

ORGANISM Branchiostoma floridae

Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

Branchiostoma.

```

REFERENCE
AUTHORS Fujiyama,A., Toyoda,A., Hattori,M. and Sakaki,Y.
TITLE BAC end sequences of CHORI-302 Amphioxus Library
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 501)
AUTHORS Fujiyama,A.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:afujiyam@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
PRIMERS
COMMENT Sequencing : TJ
LIBRARY Vector : pTARBAC2.1
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES Location/Qualifiers
source 1..501
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
/clone="CH302-032P18.R"
/sex="male"
/tissue_type="sperm"
/clone_lib="CHORI0302 Amphioxus genomic BAC library"
/note="Common name:amphioxus"
ORIGIN
Query Match 81.0%; Score 17; DB 11; Length 501;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTGTGAGGAACCTCTGT 19
|||||
DB 140 CCTGTGAGGATCTTCTGT 158
|||||
RESULT 44
LOCUS BW801116 511 bp mRNA linear EST 23-MAY-2005
DEFINITION BW801116 Amphioxus Branchiostoma floridae unpublished cDNA library,
larva whole animal Branchiostoma floridae cDNA clone bblv020j14 5',
mRNA sequence.
ACCESSION BW801116
VERSION BW801116.1 GI:66409332
KEYWORDS Branchiostoma floridae (Florida lancelet)
SOURCE Branchiostoma floridae
ORGANISM Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
REFERENCE 1 (bases 1 to 511)
AUTHORS Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
TITLE Expressed genes in Branchiostoma floridae
JOURNAL Unpublished (2005)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1..511
/organism="Branchiostoma floridae"
/mol_type="mRNA"
/db_xref="taxon:7739"
/clone="bblv020j14"
/tissue_type="whole animal"
/dev_stage="larva"
/clone_lib="Amphioxus Branchiostoma floridae unpublished
cDNA library, larva whole animal"

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ORIGIN
Query Match 81.0%; Score 17; DB 5; Length 511;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTGTGAGGAACCTCTGT 19
|||||
DB 160 CCTGTGAGGATCTTCTGT 178
|||||
RESULT 45
LOCUS CW315697 514 bp DNA linear GSS 31-OCT-2004
DEFINITION 104 806 11472500 148 35828 066 Sorghum methylation filtered library
(LiBID: 104) Sorghum bicolor genomic clone 11472500, genomic survey
sequence.
ACCESSION CW315697
VERSION CW315697.1 GI:55031885
KEYWORDS Sorghum bicolor (sorghum)
SOURCE Sorghum bicolor
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 514)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., Korf,I.F.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddaloeh,J.A. and
Martienssen,R.A.
TITLE Sorghum genome sequencing by methylation filtration
JOURNAL PLoS Biol. 3 (1), e13 (2005)
PUBMED 15660154
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 806 row: 0 column: 20
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 514.
FEATURES Location/Qualifiers
source 1..514
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11472500"
/clone_lib="Sorghum methylation filtered library (LiBID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site:1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."
ORIGIN
Query Match 81.0%; Score 17; DB 10; Length 514;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 CTGTGAGGAACCTCTGTCT 21
|||||
DB 207 CTGTGAGGAACTACTGTTT 189
|||||
RESULT 46
LOCUS DE024899 542 bp DNA linear GSS 06-APR-2005

```

DEFINITION	Branchiostoma floridae DNA, clone: CH302-039J07.F, genomic survey sequence.
ACCESSION	DE024899
VERSION	DE024899.1 GI:62268369
KEYWORDS	GSS
SOURCE	Branchiostoma floridae (Florida lancelet)
ORGANISM	Branchiostoma floridae
REFERENCE	1 Fujiyama, A., Toyoda, A., Hattori, M. and Sakaki, Y. BAC end sequences of CH0R1-302 Amphioxus Library Published Only in Database (2005)
AUTHORS	2 (bases 1 to 542)
JOURNAL	Direct Submission
TITLE	Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: afujiyam@gsc.riken.jp, URL: http://hgp.gsc.riken.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT	PRIMERS Sequencing : T7
LIBRARY	Vector : pTARBAC2.1 R.Site 1 : EcoRI R.Site 2 : EcoRI. Location/Qualifiers 1. .542
FEATURES	source /organism="Branchiostoma floridae" /mol_type="genomic DNA" /db_xref="taxon:7739" /clone="CH302-039J07.F" /sex="male" /tissue_type="sperm" /clone_lib="CH0R10302 Amphioxus genomic BAC library" /note="common name:amphioxus"
ORIGIN	Query Match 81.0%; Score 17; DB 11; Length 542; Best Local Similarity 89.5%; Pred. No. 2e+03; Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0; QY 1 CCCTGTGAGGAAGTCTCTGT 19 Db 128 CCCTGTGAGGATCTCTGT 146 RESULT 47 LOCUS CO622122 546 bp mRNA linear EST 22-JUL-2004 DEFINITION DG9-226d2 DG9-ovary Canis familiaris cDNA 3', mRNA sequence. ACCESSION CO622122 VERSION CO622122.1 GI:50525352 KEYWORDS EST. SOURCE Canis familiaris (dog) ORGANISM Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 546) Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H., Henrich, J., and Loebbert, R. Dog arrayTAG cDNA clone collection Unpublished (2004) Contact: Thomas Schlueter LION Bioscience AG Walhoferstrasse 98, D-69123 Heidelberg, Germany Tel: +49 6221 4038 150 Fax: +49 6221 4038 290 Email: Thomas.Schlueter@lionbioscience.com. Location/Qualifiers 1. .546
DEFINITION	/organism="Canis familiaris" /mol_type="mRNA" /strain="Beagle" /db_xref="taxon:9615" /tissue_type="ovary" /dev_stage="adult" /lab_host="DH10B" /clone_lib="DG9-ovary" /note="Organ: ovary; Vector: Dog pBluescript LION"
ORIGIN	Query Match 81.0%; Score 17; DB 7; Length 546; Best Local Similarity 89.5%; Pred. No. 2e+03; Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0; QY 1 CCCTGTGAGGAAGTCTCTGT 19 Db 338 CCCTCTGAGGAAGTCTCTGT 356 RESULT 48 LOCUS DN349087/c 546 bp mRNA linear EST 04-MAR-2005 DEFINITION LIB3578-029-Q1-C5 LIB3578 Canis familiaris cDNA clone ACCESSION DN349087 VERSION DN349087.1 GI:60521779 KEYWORDS EST. SOURCE Canis familiaris (dog) ORGANISM Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 546) Staten, N.R. Direct Submission (Staten, N.R.) Unpublished (2005) Contact: Nick Staten Tel: 636 247 6855 Email: nicholas.r.staten@pfizer.com. Location/Qualifiers 1. .546 /organism="Canis familiaris" /mol_type="mRNA" /strain="beagle" /db_xref="taxon:9615" /clone="CLN2496029" /tissue_type="thyroid" /lab_host="DH10B" /clone_lib="LIB3578" /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Control dog thyroid size selected"
ORIGIN	Query Match 81.0%; Score 17; DB 8; Length 546; Best Local Similarity 85.0%; Pred. No. 2e+03; Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0; QY 1 CCCTGTGAGGAAGTCTCTGTC 20 Db 119 CCNTGTGAGGAAGTCTGTC 100 RESULT 49 LOCUS CA883299 547 bp mRNA linear EST 20-DEC-2002 DEFINITION B0102D04-3N NIA Mouse Neural Stem Cell (Differentiated) cDNA Library (long) Mus musculus cDNA clone NIA:B0102D04 IMAGE:30094023 3', mRNA sequence. ACCESSION CA883299 VERSION CA883299.1 GI:27334848 KEYWORDS EST. SOURCE Mus musculus (house mouse)

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L.
and Ko, M.S.H.
TITLE        Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
JOURNAL      cDNA Library (long)
COMMENT      Unpublished (2002)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0102 row: D column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 547
POLYA=Yes.

FEATURES
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    /db_xref="taxon:10090"
    /clone="NIA:B0102D04 IMAGE:30094023"
    /dev_stage="Adult"
    /lab_host="DH10B"
    /clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
    cDNA Library (long)"
    /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
    NotI; Mouse cDNA project by the Laboratory of Genetics,
    National Institute on Aging (NIA), Intramural Research
    Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
    a long-transcript enriched cDNA library (Ref. Genome Res.
    11: 1553-1558 (2001). [PMID: 11541199]). Total RNAs were
    obtained from Dr. Angelo L. Vescovi (Institute for Stem
    Cell Research, Italy). Double-stranded cDNAs were
    synthesized with an Oligo(dT) primer [Invitrogen:
    5'-pCAGTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT-3'] from
    2.0 Microgram of total RNA, treated with T4 DNA
    polymerase, and purified by ethanol-precipitation. The
    cDNAs were ligated to Lone-linker LL-Sal4, purified by
    phenol/chloroform, and separated from free linkers by
    Centricon 100. Then, the cDNAs were amplified by
    long-range high fidelity PCR using Ex Taq polymerase
    (Takara) with a primer Sal4-S. The products were purified
    by phenol/chloroform and Centricon 100. The cDNAs were
    digested with SalI and NotI enzymes and cloned into
    SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.
    coli host was transformed with the ligation mixture by the
    standard chemical method. The average insert size is about
    3.2 kb. The library was constructed by Yulan Piao."

ORIGIN
Query Match      81.0%; Score 17; DB 6; Length 547;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3  CTGTGAGGAACCTCTGCT 21
        |||||
DB      238 CTGTAGGAACCTCTGCT 256

RESULT 50
AQ924133
LOCUS
DEFINITION
AQ924133
ACCESSION
VERSION
KEYWORDS
AQ924133.1 GI:6613136
GSS.

SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.

FEATURES
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    /db_xref="taxon:10090"
    /clone="RPCI-23-294M20"
    /sex="Female"
    /lab_host="DH10B"
    /clone_lib="RPCI-23"
    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
    EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
    brain genomic DNA was isolated and partially digested
    with a combination of EcoRI and EcoRI MethyIase. Size
    selected DNA was cloned into the pBACe3.6 vector at the
    EcoRI sites. The ligation products were transformed into
    DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
Query Match      81.0%; Score 17; DB 9; Length 556;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2  CCTGTGAGGAACCTCTGTC 20
        |||||
DB      233 CCTGTGAGGAACCTCTGTC 251

Search completed: January 27, 2006, 07:06:29
Job time : 1562.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 03:51:38 ; Search time 218.5 Seconds
(without alignments)
640.543 Million cell updates/sec

Title: US-10-070-415A-1
Perfect score: 21
Sequence: 1 cccgtgagggaactwctgtct 21
Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_21:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	98.1	21	10	ABX08667
C 2	20.6	98.1	21	12	ADJ38963 Pathogeni
C 3	20.6	98.1	21	14	ADY75041 Hepatitis
4	20.6	98.1	23	12	ADJ38943 Hepatitis
5	20.6	98.1	23	14	ADY75021 Hepatitis
6	20.6	98.1	24	2	AAK60947 Hepatitis
7	20.6	98.1	24	6	ABK88459 Hepatitis
8	20.6	98.1	25	3	AAZ99212 Primer fo
9	20.6	98.1	25	13	ADS34692 Primer Ds
10	20.6	98.1	27	2	AAQ68058 Hepatitis
C 11	20.6	98.1	27	2	AAQ68058 Hepatitis
12	20.6	98.1	27	4	AAH44980 HCV speci
13	20.6	98.1	27	4	AAH75858 Mycobacte
14	20.6	98.1	27	6	ABN79962 Hepatitis
15	20.6	98.1	28	2	AAQ05239 Hepatitis
C 16	20.6	98.1	28	3	AAZ57748 Hepatitis
17	20.6	98.1	28	3	AAZ57779 Hepatitis
18	20.6	98.1	28	14	ADV04753 Synthetic
19	20.6	98.1	28	14	ADV04766 Synthetic

C 20	20.6	98.1	45	2	AAT09176
C 21	20.6	98.1	45	2	AAV20717
C 22	20.6	98.1	45	2	AAV05026
C 23	20.6	98.1	45	2	AAV22769
C 24	20.6	98.1	45	2	ABK86838
C 25	20.6	98.1	45	8	AAQ56315
C 26	20.6	98.1	45	12	ADQ74915
C 27	20.6	98.1	45	14	ABE17467
C 28	20.6	98.1	45	14	ABE54511
C 29	20.6	98.1	51	2	AAQ533262
C 30	20.6	98.1	67	3	AAZ57776
31	20.6	98.1	70	13	ADW39164
32	20.6	98.1	73	6	AAQ40115
C 33	20.6	98.1	79	13	ADW39166
34	20.6	98.1	80	12	ADP20411
35	20.6	98.1	85	6	AAQ33033
36	20.6	98.1	95	13	ADW39165
37	20.6	98.1	103	13	ADQ05701
38	20.6	98.1	110	12	ADP87783
39	20.6	98.1	127	6	ABX03545
40	20.6	98.1	131	14	ADW15169
41	20.6	98.1	131	14	ADW15171
42	20.6	98.1	131	14	ADW15170
43	20.6	98.1	131	14	ADW15174
44	20.6	98.1	131	14	ADW15172
45	20.6	98.1	131	14	ADW15173
46	20.6	98.1	133	3	AAZ57175
C 47	20.6	98.1	155	3	AAZ57775
48	20.6	98.1	210	13	ADQ05716
49	20.6	98.1	235	13	ADQ05719
50	20.6	98.1	242	2	AAQ37774
C 51	20.6	98.1	260	3	AAZ57774
52	20.6	98.1	265	14	ADW15166
53	20.6	98.1	266	14	ADW15165
54	20.6	98.1	267	6	ABN79975
55	20.6	98.1	278	6	ABN79973
56	20.6	98.1	290	13	ADQ05722
57	20.6	98.1	297	4	AAH75861
58	20.6	98.1	299	10	AAZ55565
59	20.6	98.1	305	2	AAH79088
60	20.6	98.1	305	6	ABN79971
61	20.6	98.1	305	6	ABN79969
62	20.6	98.1	305	6	ABN79972
63	20.6	98.1	305	6	ABN79970
64	20.6	98.1	305	6	ABN79974
65	20.6	98.1	306	2	AAQ67079
66	20.6	98.1	308	3	AAZ5294
67	20.6	98.1	308	12	ADN35973
68	20.6	98.1	310	6	ABK70877
69	20.6	98.1	312	3	AAZ36198
70	20.6	98.1	314	3	AAZ36197
71	20.6	98.1	323	6	ABK70883
72	20.6	98.1	323	6	ABK70882
73	20.6	98.1	323	14	ADX58606
74	20.6	98.1	326	6	ABK70880
75	20.6	98.1	327	3	AAZ36199
76	20.6	98.1	327	6	ABK70884
77	20.6	98.1	328	6	ABL46276
78	20.6	98.1	328	6	ABL46275
79	20.6	98.1	328	6	ABL46278
80	20.6	98.1	328	6	ABL46273
81	20.6	98.1	328	8	AAZ53724
82	20.6	98.1	328	8	AAZ49656
83	20.6	98.1	329	6	ABK70871
84	20.6	98.1	332	2	AAQ75226
85	20.6	98.1	332	6	ABK70878
86	20.6	98.1	333	6	ABK70881
87	20.6	98.1	333	6	ABK70867
88	20.6	98.1	333	6	ABK70879
89	20.6	98.1	333	6	ABK70876
90	20.6	98.1	334	2	AAQ98272
91	20.6	98.1	334	6	ABK70869
92	20.6	98.1	335	6	ABK70868

Aat09176	Hepatitis
Aav20717	Hepatitis
Aav05026	Probe PA
Aav22769	Capture/A
Abk86838	Hepatitis
Aad56315	Hepatitis
Adq74915	HCV Captu
Aeb17467	HCV 5'UTR
Aeb54511	HCV detec
Aag53262	Hepatitis
Aaz57776	Hepatitis
Adw39164	Novel nuc
Aal40115	Pathogeni
Adw39166	Novel nuc
Adp20411	Hepatitis
Aad33033	HCV-s1 ov
Adw39165	Novel nuc
Adr05701	Hepatitis
Adp87783	Hepatitis
Abx03545	Hepatitis
Adw15169	HCV H77C
Adw15171	HCV from
Adw15170	HCV from
Adw15174	HCV from
Adw15172	HCV from
Adw15173	HCV from
Aaz57175	Human hep
Aaz57775	Hepatitis
Adr05716	Hepatitis
Adr05719	Hepatitis
Aaq37774	Cloned HC
Aaz57774	Hepatitis
Adw15166	HCV RT-PC
Adw15165	HCV H77C
Abn79975	Hepatitis
Abn79973	Hepatitis
Adr05722	Hepatitis
Aah75861	Mycobacte
Aad55565	IG57272 H
Aat87088	HCV ampli
Abn79971	Hepatitis
Abn79969	Hepatitis
Abn79972	Hepatitis
Abn79970	Hepatitis
Abn79974	Hepatitis
Aaq67079	Hepatitis
Aaa75294	Novel hep
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Abk70877	HCV genom
Aaz36198	Adapted H
Aaz36197	HCV genom
Abk70883	HCV genom
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Abk70880	HCV genom
Aaz36199	Adapted H
Abk70884	HCV genom
Abi46276	Hepatitis
Abi46275	Hepatitis
Abi46278	Hepatitis
Abi46273	Hepatitis
Aal53724	Human int
Aad49656	Human int
Abk70871	HCV genom
Aaq75226	Hepatitis
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Abk70881	HCV genom
Abk70867	HCV genom
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Abk70876	HCV genom
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Abk70869	HCV genom
Abk70868	HCV genom

93 Abk70885 HCV genom
94 Abk70874 HCV genom
95 Abk70870 HCV genom
96 Adr05731 Hepatitis
97 Adr05688 Hepatitis
98 Abk70886 HCV genom
99 Adv04744 Synthetic
100 Adv04743 Synthetic

Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACACTWCTGTCT 21
Db 1 CCTGTGAGGAACACTWCTGTCT 21

RESULT 2

ADJ38963/c
ID ADJ38963 standard; RNA; 21 BP.

XX AC ADJ38963;

XX DT 06-MAY-2004 (first entry)

XX DE Hepatitis C virus siRNA antisense oligonucleotide 5U8.

XX KW small interfering RNA; siRNA; modified ribonucleotide;

XX KW viral replication inhibition; hepatitis C virus; HCV; hepatitis C;

XX KW antiinflammatory; hepatotropic; virucide; hepatitis A virus;

XX KW hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;

XX KW rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus;

XX KW metapneumoniavirus; coronavirus; viral infection; ss.

XX OS Hepatitis C virus.

XX OS Synthetic.

XX PN WO2004011647-A1.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023104.

XX PR 26-JUL-2002; 2002US-0398505P.

XX PA (CHIR) CHIRON CORP.

XX PI Han J, Seo MY, Houghton M;

XX WI MPI; 2004-143862/14.

XX PT New RNase resistant small interfering RNA, useful for treating viral
infections, e.g., hepatitis C, influenza virus or coronavirus infection.

XX PS Example 12; Fig 2; 74pp; English.

XX CC The present invention describes a small interfering RNA (siRNA) which
comprises a modified ribonucleotide, where the siRNA is resistant to
RNase and retains the ability to inhibit viral replication. Also
described: (1) inactivating a virus in a patient; (2) making a modified
siRNA that targets a nucleic acid sequence in a virus; (3) a double-
stranded RNA molecule of 10-30 nucleotides that inhibits replication of
hepatitis C virus (HCV); (4) inducing targeted RNA interference toward
HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector
comprising a DNA segment encoding the RNA molecule; (7) a host cell
comprising the vector of (6); (8) inhibiting replication of HCV in cells
carrying HCV; (9) treating hepatitis C in a subject; (10) a modified
siRNA molecule comprising a double-stranded RNA molecule of 10-30
nucleotides in length, which mediates RNA interference toward a target
agent or virus and is linked to at least one receptor-binding ligand; and
CC (11) inducing targeted RNA interference in a patient. The modified siRNA
molecules have antiinflammatory, hepatotropic and virucide activities.
The modified RNA molecules are useful for inactivating virus in mammalian
cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A
virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza
virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma
virus, metapneumoniavirus or coronavirus infections. The methods of the
invention can be used to correct or compensate for cellular physiological
abnormalities involved in conferring susceptibility to viral infections.
in patients and/or alleviate symptoms of a viral infection in patients.
The present sequence represents an siRNA oligonucleotide, which is used
in an example from the present invention.

ALIGNMENTS

RESULT 1

ABX08667

ID ABX08667 standard; DNA; 21 BP.

XX AC ABX08667;

XX DT 20-JAN-2003 (first entry)

XX DE Pathogenic organism detection method associated PCR primer #1.

XX KW PCR; primer; ss; hepatitis C virus; human; pathogenic microorganism;

XX KW influenza; AIDS; acquired immunodeficiency syndrome.

XX OS Hepatitis C virus.

XX PN WO20027281-A1.

XX PD 03-OCT-2002.

XX PF 05-MAR-2002; 2002WO-JF002030.

XX PR 27-MAR-2001; 2001JP-00090053.

XX PR 18-SEP-2001; 2001JP-00284112.

XX PA (TOKE) TOSHIBA KK.

XX PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;

XX WI MPI; 2003-040593/03.

XX PT Detecting nucleic acids relating diseases particularly due to pathogenic
microorganisms e.g. hepatitis, influenza and AIDS in individuals from
their data using immobilized probes on substrate, also for therapeutic
evaluation.

XX PS Claim 16; Page 83; 125pp; Japanese.

XX CC This invention relates to a method for obtaining first data on a nucleic
acid from an individual exposed to a specific disease and second data on
a nucleic acid from a pathogenic microorganism occurring in the
individual in order to relate the specific disease to such pathogenic
microorganism. The method of the invention comprises the reaction of a
nucleic acid extract from the individual with a probe-immobilization
substrate containing first and second probes for detection of the
pathogenic microorganism with the first probe to relate to the specific
microbe-caused disease, and the second probe for detecting a specific
nucleic acid in the individual and obtaining first data from the reaction
results as well as the detected binding of a nucleic acid with the first
probe and/or second data from the detected binding of a nucleic acid with
the second probe. The method of the invention is useful for detecting
nucleic acids relating diseases particularly due to pathogenic
microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
also for therapeutic evaluation. Such a method is convenient and accurate
and may be used to design specific therapy for effective treatment even
for individual patients in a tailor-made manner. The present sequence
represents a PCR primer used in the method of the invention

XX SQ Sequence 21 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 1 Other;

XX Query Match 98.1%; Score 20.6; DB 10; Length 21;

XX SQ Sequence 21 BP; 6 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 12; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.2;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGTGAGGAAGTCTGTCT 21
|||||:|||||:|||||
Db 21 CCTGTGAGGAAGTCTGTCT 1

RESULT 3
ADY75041/c
ID ADY75041 standard; RNA; 21 BP.
XX AC ADY75041;
XX DT 02-JUN-2005 (first entry)
XX DE Hepatitis C virus antisense siRNA508 oligo targeted to 5' UTR Seq 30.
XX KW virus inactivation; RNA interference; short interfering RNA; siRNA;
XX KW gene silencing; gene therapy; antiinflammatory; hepatotropic; virucide;
XX KW viral infection; hepatitis C virus infection; ss;
XX KW antisense oligonucleotide.
XX OS Hepatitis C virus.
XX US2005058982-A1.
XX PN 17-MAR-2005.
XX PD 25-JUL-2003; 2003US-00626879.
XX PF 26-JUL-2002; 2002US-0398605P.
XX PR 11-APR-2003; 2003US-0461838P.
XX PR 14-MAY-2003; 2003US-0470230P.
XX PA (CHIR) CHIRON CORP.
XX PI Han J, Seo M, Houghton M;
XX WPI; 2005-222217/23.
XX DR
XX PT Inactivating a virus (e.g. HCV) in a patient to treat the viral infection
XX PT comprises administering to the patient a modified small interfering RNA
XX PT in an amount to inactivate the virus.
XX PS Disclosure; SEQ ID NO 30; 60pp; English.
XX CC This invention relates to a novel method for inactivating a virus in a
XX CC patient. Specifically, it refers to the administration of a modified
XX CC small interfering RNA (siRNA) in an amount suitable to inactivate the
XX CC virus, where the siRNA comprises a modified ribonucleotide that is
XX CC resistant to RNase and retains the ability to inhibit viral replication.
XX CC In particular, it refers to double-stranded RNA (dsRNA) molecules of
XX CC about 10-30 nucleotides in length that can inhibit replication of the
XX CC hepatitis C virus (HCV) by gene specific suppression of expression,
XX CC especially in hepatic cells. The present invention, however, also
XX CC describes the inactivation of a virus chosen from hepatitis A virus,
XX CC hepatitis B virus, hepatitis D virus, hepatitis E virus, Ebola virus,
XX CC influenza virus, rotavirus, reovirus, poliovirus, human
XX CC papilloma virus, metapneumovirus or coronavirus. The siRNA is prepared by
XX CC identifying a target nucleotide sequence in a virus genome that is
XX CC necessary for replication and producing a 2' modified siRNA that will
XX CC bind to this region, where the 2' modification is chosen from fluoro-,
XX CC methyl-, methoxyethyl- or propyl-modification. As such, these siRNA
XX CC molecules and compositions derived thereof can be used in gene therapy
XX CC and exhibit antiinflammatory, hepatotropic and virucide activities. The
XX CC composition and methods are useful for treating viral infections, such as
XX CC HCV infections. This oligonucleotide sequence is a Hepatitis C virus
XX CC siRNA oligo of the invention.

XX SQ Sequence 21 BP; 6 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 14; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.2;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGTGAGGAAGTCTGTCT 21
|||||:|||||:|||||
Db 21 CCTGTGAGGAAGTCTGTCT 1

RESULT 4
ADJ38943
ID ADJ38943 standard; RNA; 23 BP.
XX AC ADJ38943;
XX DT 06-MAY-2004 (first entry)
XX DE Hepatitis C virus siRNA target oligonucleotide 508.
XX KW small interfering RNA; siRNA; modified ribonucleotide;
XX KW viral replication inhibition; hepatitis C virus; HCV; hepatitis C;
XX KW antiinflammatory; hepatotropic; virucide; hepatitis A virus;
XX KW hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;
XX KW rotavirus; reovirus; poliovirus; human papilloma virus;
XX KW metapneumovirus; coronavirus; viral infection; target; ss.
XX OS Hepatitis C virus.
XX OS Synthetic.
XX PN WO2004011647-A1.
XX XX 05-FEB-2004.
XX PD 25-JUL-2003; 2003WO-US023104.
XX PF 26-JUL-2002; 2002US-0398605P.
XX PR (CHIR) CHIRON CORP.
XX PA Han J, Seo MY, Houghton M;
XX PI WPI; 2004-143862/14.
XX DR
XX PT New RNase resistant small interfering RNA, useful for treating viral
XX PT infections, e.g., hepatitis C, influenza virus or coronavirus infection.
XX PS Example 12; Fig 2; 74pp; English.
XX CC The present invention describes a small interfering RNA (siRNA) which
XX CC comprises a modified ribonucleotide, where the siRNA is resistant to
XX CC RNase and retains the ability to inhibit viral replication. Also
XX CC described: (1) inactivating a virus in a patient; (2) making a modified
XX CC siRNA that targets a nucleic acid sequence in a virus; (3) a double-
XX CC stranded RNA molecule of 10-30 nucleotides that inhibits replication of
XX CC hepatitis C virus (HCV); (4) inducing targeted RNA interference toward
XX CC HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector
XX CC comprising a DNA segment encoding the RNA molecule; (7) a host cell
XX CC comprising the vector of (6); (8) inhibiting replication of HCV in cells
XX CC carrying HCV; (9) treating hepatitis C in a subject; (10) a modified
XX CC siRNA molecule comprising a double-stranded RNA molecule of 10-30
XX CC nucleotides in length, which mediates RNA interference toward a target
XX CC agent or virus and is linked to at least one receptor-binding ligand; and
XX CC (11) inducing targeted RNA interference in a patient. The modified siRNA
XX CC molecules have antiinflammatory, hepatotropic and virucide activities.
XX CC The modified RNA molecules are useful for inactivating virus in mammalian
XX CC cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A
XX CC virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza
XX CC virus, rotavirus, reovirus, poliovirus, poliovirus, human papilloma
XX CC virus, metapneumovirus or coronavirus infections. The methods of the
XX CC invention can be used to correct or compensate for cellular physiological

CC abnormalities involved in conferring susceptibility to viral infections
 CC in patients and/or alleviate symptoms of a viral infection in patients.
 CC The present sequence represents an siRNA target oligonucleotide, which is
 CC used in an example from the present invention.

XX
 SQ Sequence 23 BP; 4 A; 7 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 12; Length 23;
 Best Local Similarity 66.7%; Pred. No. 3.3;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
 |||:|||||:|||||:|:|:
 Db 1 CCCUGUGAGGAACUACUGUCU 21

RESULT 5
 ADY75021
 ID ADY75021 standard; RNA; 23 BP.
 XX
 AC ADY75021;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Hepatitis C virus RNA target of a viral inactivating siRNA duplex Seq 10.
 XX
 KW virus inactivation; RNA interference; gene silencing; gene therapy;
 KW antiinflammatory; hepatotropic; virucide; viral infection;
 KW hepatitis C virus infection; ss.

OS Hepatitis C virus.
 XX
 US2005058982-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 25-JUL-2003; 2003US-00626879.

XX
 PR 26-JUL-2002; 2002US-0398605P.
 PR 11-APR-2003; 2003US-0461838P.
 PR 14-MAY-2003; 2003US-0470230P.
 XX
 PA (CHIR) CHIRON CORP.

XX
 PI Han J, Seo M, Houghton M;
 XX
 DR WPI; 2005-222217/23.

XX
 PT Inactivating a virus (e.g. HCV) in a patient to treat the viral infection
 PT comprises administering to the patient a modified small interfering RNA
 PT in an amount to inactivate the virus.

PS Disclosure; SEQ ID NO 10; 60pp; English.

XX
 CC This invention relates to a novel method for inactivating a virus in a
 CC patient. Specifically, it refers to the administration of a modified
 CC small interfering RNA (siRNA) in an amount suitable to inactivate the
 CC virus, where the siRNA comprises a modified ribonucleotide that is
 CC resistant to RNase and retains the ability to inhibit viral replication.
 CC In particular, it refers to double-stranded RNA (dsRNA) molecules of
 CC about 10-30 nucleotides in length that can inhibit replication of the
 CC hepatitis C virus (HCV) by gene specific suppression of expression,
 CC especially in hepatic cells. The present invention, however, also
 CC describes the inactivation of a virus chosen from hepatitis A virus,
 CC hepatitis B virus, hepatitis D virus, hepatitis E virus, Ebola virus,
 CC influenza virus, rotavirus, reovirus, retrovirus, poliovirus, human
 CC papilloma virus, metapneumovirus or coronavirus. The siRNA is prepared by
 CC identifying a target nucleotide sequence in a virus genome that is
 CC necessary for replication and producing a 2' modified siRNA that will
 CC bind to this region, where the 2' modification is chosen from fluoro-,
 CC methyl-, methoxyethyl- or propyl-modification. As such, these siRNA
 CC molecules and compositions derived thereof can be used in gene therapy
 CC and exhibit antiinflammatory, hepatotropic and virucide activities. The

CC composition and methods are useful for treating viral infections, such as
 CC HCV infections. This oligonucleotide sequence is a Hepatitis C virus RNA
 CC oligo, target of an siRNA duplex that inhibits viral replication, given
 CC in an exemplification of the invention.

XX
 SQ Sequence 23 BP; 4 A; 7 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 23;
 Best Local Similarity 66.7%; Pred. No. 3.3;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
 |||:|||||:|||||:|:|:
 Db 1 CCCUGUGAGGAACUACUGUCU 21

RESULT 6
 AAX60947
 ID AAX60947 standard; DNA; 24 BP.
 XX
 AC AAX60947;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Hepatitis C virus (HCV) primer HCVC.

XX
 KW Nucleic acid detection; pathogen; bacteria; virus; hepatitis C virus;
 KW HCV; hepatitis B; HBV; hepatitis G; HGV; HIV; fungus; protozoa; ss;
 KW parasite; mycoplasma; genetic mutation; food contamination; PCR primer.

XX
 OS Synthetic.
 OS Hepatitis C virus.

XX
 PN WO9928503-A1.
 XX
 PD 10-JUN-1999.

XX
 PF 16-NOV-1998; 98WO-US024494.
 XX
 PR 03-DEC-1997; 97IT-RM000749.

XX
 PA (DIAS-) DIASORIN INT INC.

XX
 PI Primi D, Mantero G;

XX
 DR WPI; 1999-371139/31.

XX
 PT Detection of single-stranded polynucleotide analytes.

XX
 PS Claim 53; Page 65; 73pp; English.

XX
 CC The invention relates to a new method for detection of single-stranded
 CC (ss) polynucleotide analytes that comprises using ss polynucleotide
 CC probes which hybridize to the analyte and are bound to a solid support
 CC where double-stranded (ds) polynucleotides are detected. The method can
 CC be used for detecting ss PN analytes for the detection of pathogens such
 CC as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV),
 CC hepatitis G (HGV), or HIV, fungi, protozoa, parasites or mycoplasma. The
 CC method can be used to detect the presence of genetic mutations which have
 CC diagnostic or prognostic value. Pathogen contamination of food and drink
 CC supplies can also be detected using the method. The method provides for
 CC the sensitive and specific detection of ss PN analytes at concentration
 CC as low as 0.1fg

XX
 SQ Sequence 24 BP; 4 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 2; Length 24;
 Best Local Similarity 95.2%; Pred. No. 3.3;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
 |||:|||||:|||||:|:|:
 Db 2 CCCTGTGAGGAACACTGTGTCT 22

RESULT 7
ID ABK88459 standard; DNA; 24 BP.
XX AC ABK88459;
XX DT 07-OCT-2002 (first entry)
XX DE Hepatitis C virus forward PCR primer CTL1.f.
XX KW HCV; PCR; primer; ss; CTL1.f; internal control; human parvovirus;
XX KW 5' nuclease polymerase chain reaction assay; hepatitis A virus;
XX KW human immunodeficiency virus; hepatitis B virus.
XX OS Hepatitis C virus.
XX PN WO200252041-A2.
XX PD 04-JUL-2002.
XX PF 19-DEC-2001; 2001WO-EP015069.
XX PR 22-DEC-2000; 2000US-00746874.
XX PA (BAXT) BAXTER AG.
XX PI Gessner M;
XX DR WPI; 2002-575389/61.
XX PT 5' nuclease polymerase chain reaction assay, useful for detecting
XX PT pathogens, e.g. HIV or hepatitis virus, comprises employing an internal
XX PT control probe having a nucleic acid to the inverted target
XX PT oligonucleotide probe binding site.
XX PS Example 1; Page 23; 37pp; English.
XX CC The invention relates to a 5' nuclease polymerase chain reaction (PCR)
XX CC assay having an internal control comprising an oligonucleotide having as
XX CC part of its sequence an inverse of a target oligonucleotide probe binding
XX CC site nucleic acid sequence, and an internal control probe having a
XX CC nucleic acid sequence complementary to the inverted target
XX CC oligonucleotide probe binding site. Also included is a hepatitis C virus
XX CC (HCV) 5' nuclease PCR assay comprising: (a) a first probe having a first
XX CC detectable label and a nucleic acid sequence complementary to a target
XX CC HCV oligonucleotide probe binding sequence; (b) a 5' nuclease enzyme; (c)
XX CC a second probe having a second detectable label and having a nucleic acid
XX CC sequence complementary to an internal standard oligonucleotide probe
XX CC binding sequence, where the internal standard oligonucleotide probe
XX CC binding sequence is the inverse of the target HCV oligonucleotide probe
XX CC binding sequence; (d) at least one primer complementary to primer binding
XX CC sites on the target HCV nucleotide and the internal standard
XX CC oligonucleotide; and (e) at least one primer complementary to primer
XX CC binding sites on the target HCV nucleotide. The 5' nuclease PCR assay is
XX CC useful for detecting pathogens such as human immunodeficiency viruses
XX CC (HIV), hepatitis C virus, hepatitis B virus, human parvovirus and
XX CC hepatitis A virus, as well as non-viral pathogens. The method is also
XX CC used for quick and accurate determination of optimum nucleic acid
XX CC sequences for use as internal amplification controls in 5' nuclease PCR
XX CC assays. The internal control is used to detect nucleic acid amplification
XX CC assay corruption, and to verify assay performance. The present sequence
XX CC is an HCV PCR primer used to demonstrate the method of the invention
XX SQ Sequence 24 BP; 5 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 6; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

Db 1 CCCTGTGAGGAAGTCTGTCT 21
RESULT 8
AAZ99212
ID AAZ99212 standard; DNA; 25 BP.
XX AC AAZ99212;
XX DT 19-JUN-2000 (first entry)
XX DE Primer for primer-specific and mispair extension analysis of HCV.
XX KW Primer-specific and mispair extension assay; PSMEA;
XX KW genotype determination; HCV; gene variation; PCR primer; ss.
XX OS Hepatitis C virus.
XX PN WO200009745-A1.
XX PD 24-FEB-2000.
XX PF 09-AUG-1999; 99WO-CA000733.
XX PR 13-AUG-1998; 98CA-02245039.
XX PA (CABL-) CANADIAN BLOOD SERVICES.
XX PA (HEMA-) HEMA-QUEBEC.
XX PI Hu Y;
XX DR WPI; 2000-224367/19.
XX PT Primer-specific and mispair extension assay for identifying gene
XX PT variations, comprises specific primer amplification of unknown nucleic
XX PT acid sequences of patients using incomplete dNTP sets.
XX PS Disclosure; Page 13; 65pp; English.
XX CC AAZ99212-26 represent PCR primers used in a primer-specific and mispair
XX CC extension assay (PSMEA) for genotype determination of Hepatitis C virus
XX CC (HCV). The method comprises extending an unknown nucleic acid sequence
XX CC (from a patient) using a primer specific for particular genotype and
XX CC incomplete set of dNTPs under suitable conditions followed by
XX CC characterizing and comparing the extension products with known nucleic
XX CC acid sequences of various genotypes. The present primers are used for
XX CC detecting nucleotide variations in the 5' untranslated region of the HCV
XX CC genome. PSMEA is capable of accurately detecting heterozygotes and
XX CC nucleotide mutations in a nucleic acid sequence. The PSMEA is useful for
XX CC identifying gene variations such as in different genotypes or subtypes of
XX CC a given genotype, especially Hepatitis C virus genotypes and subtypes
XX SQ Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 3; Length 25;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
Db 4 CCCTGTGAGGAAGTCTGTCT 24
|||||
RESULT 9
ADS34692
ID ADS34692 standard; DNA; 25 BP.
XX AC ADS34692;
XX DT 02-DEC-2004 (first entry)
XX PR Primer Ds5-41-S25, seq id 35.
XX

KW Virucide; antiinflammatory; hepatotropic; hepatitis C virus; HCV;
 KW proliferation; siRNA; short interfering RNA; RNA interference;
 KW gene silencing; PCR; primer; ss.
 XX
 XX Unidentified.
 OS
 XX WO2004078974-A1.
 PN
 XX 16-SEP-2004.
 PD
 XX 23-JAN-2004; 2004WO-JP000605.
 PF
 XX 24-JAN-2003; 2003JP-00016750.
 PR
 XX (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Kohara M, Watanabe T, Taira K, Miyagishi M, Sudo M;
 PI WPI; 2004-662428/64.
 XX
 DR New oligo ribonucleotide or peptide nucleic acid capable of sequence-
 XX specifically binding with RNA of hepatitis C virus, useful for inhibiting
 XX proliferation of hepatitis C virus and useful as hepatitis C virus
 PT therapeutic agent.
 PT
 XX Example 6; SEQ ID NO 35; 80pp; Japanese.
 PS
 XX The invention relates to an oligo ribonucleotide or peptide nucleic acid
 CC (I) capable of sequence-specifically binding with RNA of hepatitis C
 CC virus (HCV), and comprising a sequence hybridising under stringent
 CC conditions with RNA of HCV. The method of the invention relates to the
 CC inhibition of the proliferation of HCV. The oligo ribonucleotide or
 CC peptide nucleic acid of the invention is useful for inhibiting the
 CC proliferation of HCV which involves contacting (I) with RNA of HCV. (I)
 CC is useful as a therapeutic agent of hepatitis C. The current sequence
 CC represents a primer used in an example from the invention.
 XX
 XX Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 98.1%; Score 20.6; DB 13; Length 25;
 Best Local Similarity 95.2%; Pred. No. 3.3;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTGTGAGGAAGTCTGCT 21
 Db 5 CCCTGTGAGGAAGTCTGCT 25
 RESULT 10
 AAQ68058
 ID AAQ68058 standard; DNA; 27 BP.
 XX
 AC AAQ68058;
 XX
 XX 25-MAR-2003 (revised)
 DT 19-DEC-1994 (first entry)
 DT
 DE Primer Hcp98 for HCV genotyping (universal).
 XX
 XX Hepatitis C virus; HCV; probe; genotyping; hybridisation;
 KW non-A, non-B hepatitis; NANBH; amplification; primer;
 KW polymerase chain reaction; PCR; ss.
 XX
 XX Synthetic.
 OS
 XX WO9412670-A2.
 PN
 XX 09-JUN-1994.
 PD
 XX 26-NOV-1993; 93WO-EP003325.
 PF
 XX 27-NOV-1992; 92EP-00403222.
 PR

PR 31-AUG-1993; 93EP-00402129.
 XX (INNO-) INNOGENETICS NV SA.
 PA
 PI Maertens G, Stuyver L, Rossau R, Van Heuverswyn H;
 XX WPI; 1994-200296/24.
 DR
 XX Process for genotyping Hepatitis C virus (HCV) isolates - utilises probes
 PT hybridising to HCV isolate domains.
 PT
 XX Claim 13; Page 73; 96pp; English.
 PS
 XX Genotyping HCV utilises probes hybridising to HCV isolate domains. HCV
 CC types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b, 3c, 4a, 4b,
 CC 4c, 4d, 4e, 4f, 4g and 4h can be typed. The hybridisation step is pref.
 CC preceded by an amplification step (PCR) using universal primers given in
 CC AAQ68058-61. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 27 BP; 4 A; 9 C; 6 G; 7 T; 0 U; 1 Other;
 SQ
 Query Match 98.1%; Score 20.6; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTGTGAGGAAGTCTGCT 21
 Db 1 CCCTGTGAGGAAGTCTGCT 21
 RESULT 11
 AAQ05212/c
 ID AAQ05212 standard; DNA; 27 BP.
 XX
 AC AAQ05212;
 XX
 DT 13-JUN-1996 (first entry)
 DT
 XX Hepatitis C virus antisense oligonucleotide A65.
 DE
 XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
 KW infection; antisense; non coding; region; NCR; core region; ss.
 XX
 OS Synthetic.
 XX
 XX WO9530746-A1.
 PN
 XX 16-NOV-1995.
 PD
 XX 08-MAY-1995; 95WO-US005812.
 PF
 XX 10-MAY-1994; 94US-00240382.
 PR
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 XX Wakita T, Wands JR;
 PI
 XX WPI; 1995-404113/51.
 DR
 XX New anti-sense hepatitis C virus oligo:nucleotide(s) - used for
 PT inhibiting HCV RNA translation, for the treatment or prevention of HCV
 PT infection.
 PT
 XX Claim 1; Page 26; 50pp; English.
 PS
 XX The present oligonucleotide (ON) inhibits the expression of hepatitis C
 CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis
 CC is inhibited by 74% and 54%, respectively. The ONs of the invention
 CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,
 CC and can therefore be used to treat or prevent HCV infection. The
 CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV
 CC 5'-non-coding and part of the core region. The A or S in the ONs name

CC denotes antisense or sense, and the no. indicates the position of the 5'-
CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA
XX
SQ Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 2; Length 27;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||
DB 23 CCCTGTGAGGAAGTCTGTCT 3

RESULT 12

AAH44980
ID AAH44980 standard; DNA; 27 BP.

XX
AC AAH44980;

DT 05-SEP-2001 (first entry)

DE HCV specific primer HcP-98.

XX Multiple viral agent detection; human immunodeficiency virus; HIV;
KW Hepatitis C virus; HCV; Hepatitis B virus; Hepatitis C virus; HCV;
KW blood transfusion; blood donation; viral infection; primer; ss.

OS Hepatitis C virus.

XX WO200136442-A1.

PN 25-MAY-2001.

PD 17-NOV-2000; 2000WO-US031738.

PF 17-NOV-1999; 99US-0165916P.

PR (JIJ/J) JI J.

PA (MANA/) MANAK M.

PA (WUKK/) WU K.

PA (CHEN/) CHEN X.

PA (YANG/) YANG L.

XX Ji J, Manak M, Wu K, Chen X, Yang L;

PI WPI; 2001-355605/37.

XX Simultaneous detection of HIV, HBV and HCV in samples useful to test
PT donated blood for viral infection comprises amplification of nucleic
PT acids.

PS Disclosure; Page 16; 51pp; English.

XX This invention relates to a method for detecting multiple viral agents in
CC a sample. The method consists of amplifying nucleic acids from Human
CC immunodeficiency virus (HIV), Hepatitis C virus (HCV), and or Hepatitis B
CC virus (HBV) using a mixture of primers specific for HBV, HCV HIV-1 type M
CC and HIV-1 type O and detecting their presence. Included in the invention
CC is a kit for the detection of HIV, HCV, HBV and combinations of them in a
CC blood or blood product sample. The method can be used to test blood
CC donated for transfusions for the presence of infection with HIV, HBV or
CC HCV. The present sequence represents a primer specific for HCV, which can
CC be used in the method of the invention

XX Sequence 27 BP; 4 A; 9 C; 6 G; 7 T; 0 U; 1 Other;

Query Match

Best Local Similarity 100.0%; Score 20.6; DB 4; Length 27;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

DB 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 13

AAH75858
ID AAH75858 standard; DNA; 27 BP.

XX
AC AAH75858;

DT 26-OCT-2001 (first entry)

DE Mycobacterium tuberculosis forward PCR primer p60.

XX PCR primer; ss.

OS Mycobacterium tuberculosis.

XX RU2163638-C1.

PN 27-FEB-2001.

PD 06-DEC-1999; 99RU-00125164.

PF 06-DEC-1999; 99RU-00125164.

PR (ASIB=) AS SIBE BIOCHEM RES INST.

PA Beklemishev AB, Khorosheva EM, Nomokonova N Yu;

PI WPI; 2001-280317/29.

XX Detection of DNA from tuberculosis mycobacterium complex comprising a
PT polymerase chain reaction method.

PS Claim 9; Col 17-18; 13pp; Russian.

XX The present invention relates to a PCR-based method for the detection of
CC Mycobacterium tuberculosis. The present sequence is a PCR primer for
CC Mycobacterium tuberculosis. This sequence was used to illustrate the
CC method of the present invention

XX Sequence 27 BP; 5 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 4; Length 27;

Best Local Similarity 95.2%; Pred. No. 3.3;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||

DB 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 14

ABN79962
ID ABN79962 standard; DNA; 27 BP.

XX
AC ABN79962;

DT 15-JUL-2002 (first entry)

DE Hepatitis C virus PCR primer HCV-PCR-OUTP.

XX Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KW tissue typing; PCR; primer; HCV; ss.

OS Hepatitis C virus.

XX WO2002020837-A2.

PN 14-MAR-2002.

PD 10-SEP-2001; 2001WO-GB004042.

XX

PR 08-SEP-2000; 2000GB-00022069.
 XX (PYRO-) PYROSEQUENCING PA.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (GARD/) GARDNER R.
 XX
 PI Ronaghi M, Ekstroem B, Pourmand N;
 XX WPI; 2002-393849/42.
 XX
 DR Typing nucleic acid for obtaining information about several variable
 PT sites involves simultaneously or sequentially performing two or more
 PT primer extension reactions, and determining the pattern of nucleotide
 PT incorporation.
 XX
 PS Example 1; Page 43; 86pp; English.
 XX
 CC The invention relates to a novel method for obtaining typing information
 CC about several variable sites within target nucleic acid, or typing one or
 CC more nucleic acid molecules. The methods of the invention are useful for
 CC typing one or more nucleic acid molecules containing two or more variable
 CC sites, preferably nucleic acid molecules containing three or more
 CC variable sites are typed, where three or more primer extension reactions
 CC are performed. The method is also useful for diagnosis of pathological
 CC conditions characterized by the presence of specific nucleic acid
 CC molecule(s). The methods are particularly suited for identifying
 CC microbial species or their subtypes, and in typing procedures e.g. typing
 CC of polymorphisms, tissue typing or in clinical applications. The sequence
 CC represents a PCR primer used in the invention to type hepatitis C virus
 CC (HCV) positive sera
 XX
 SQ Sequence 27 BP; 4 A; 9 C; 6 G; 7 T; 0 U; 1 Other;
 Query Match 98.1%; Score 20.6; DB 6; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTGTGAGGAACTWCTGTCT 21
 Db 1 CCTGTGAGGAACTWCTGTCT 21
 RESULT 15
 AAT05239
 ID AAT05239 standard; DNA; 28 BP.
 AC AAT05239;
 XX
 DT 13-JUN-1996 (first entry)
 XX
 DE Hepatitis C virus sense oligonucleotide S38.
 XX
 KW Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
 KW infection; sense; non coding; region; NCR; core region; ss.
 XX
 OS Synthetic.
 XX
 PN WO9530746-A1.
 XX
 PD 16-NOV-1995.
 XX
 PF 08-MAY-1995; 95WO-US005812.
 XX
 PR 10-MAY-1994; 94US-00240382.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Wakita T, Wands JR;
 XX
 DR WPI; 1995-404113/51.
 XX
 PT New anti:sense hepatitis C virus oligo:nucleotide(s) - used for

PT inhibiting HCV RNA translation, for the treatment or prevention of HCV
 PT infection.
 XX
 PS Example; Page 33; 50pp; English.
 XX
 CC The present oligonucleotide (ON) inhibits the expression of hepatitis C
 CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis
 CC is inhibited by -4% and ND, respectively. The ONs of the invention
 CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,
 CC and can therefore be used to treat or prevent HCV infection. The
 CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV
 CC 5'-non-coding and part of the core region. The A or S in the ONs name
 CC denotes antisense or sense, and the no. indicates the position of the 5'-
 CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA, and
 CC ND denotes not determined
 XX
 SQ Sequence 28 BP; 5 A; 10 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 98.1%; Score 20.6; DB 2; Length 28;
 Best Local Similarity 95.2%; Pred. No. 3.3;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTGTGAGGAACTWCTGTCT 21
 Db 6 CCTGTGAGGAACTACTGTCT 26
 RESULT 16
 AAZ57748/c
 ID AAZ57748 standard; DNA; 28 BP.
 XX
 AC AAZ57748;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Hepatitis C virus antisense inhibitor oligonucleotide A65.
 XX
 KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.
 XX
 OS Hepatitis C virus.
 XX
 PN US6001990-A.
 XX
 PD 14-DEC-1999.
 XX
 PF 07-JUN-1995; 95US-00474700.
 XX
 PR 10-MAY-1994; 94US-00240382.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Moradpour D, Wands JR, Wakita T;
 XX
 DR WPI; 2000-104900/09.
 XX
 PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
 PT Hepatitis C virus infections.
 XX
 PS Claim 3; Col 19; 31pp; English.
 XX
 CC This sequence is an antisense oligonucleotide that hybridises to
 CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
 CC invention relates to HCV antisense oligonucleotides, and also for a
 CC vector comprising a nucleotide sequence which is transcribed in an animal
 CC cell to generate an antisense oligonucleotide. The oligonucleotides have
 CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
 CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
 CC Hepatitis C virus is a positive strand RNA virus, and is the major
 CC causative agent of post-transfusion hepatitis. Persistent HCV infection
 CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
 XX
 SQ Sequence 28 BP; 8 A; 5 C; 10 G; 5 T; 0 U; 0 Other;

```

Query Match      98.1%; Score 20.6; DB 3; Length 28;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||
Db 23 CCCTGTGAGGAAGTCTGTCT 3

RESULT 17
AAZ57779
ID AAZ57779 standard; DNA; 28 BP.
XX
AC AAZ57779;
XX
DT 05-APR-2000 (first entry)
XX
DE Hepatitis C virus sense oligonucleotide S38.
XX
XX Hepatitis C virus; HCV; sense oligonucleotide; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
OS Hepatitis C virus.
XX
XX US6001990-A.
PN
XX
PD 14-DEC-1999.
XX
PF 07-JUN-1995; 95US-00474700.
XX
PR 10-MAY-1994; 94US-00240382.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
PI Moradpour D, Wands JR, Wakita T;
XX
XX WPI; 2000-104900/09.
DR
XX
XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections.
PS
XX Disclosure; Col 27; 3lpp; English.
XX
XX This sequence is an sense oligonucleotide used in the method of the
CC invention. The invention relates to hepatitis C virus (HCV) antisense
CC oligonucleotides that hybridise to HCV RNA under physiological
CC conditions. The also relates to a vector comprising a nucleotide sequence
CC which is transcribed in an animal cell to generate an antisense
CC oligonucleotide. The oligonucleotides have virucide, hepatotropic and
CC anti-inflammatory activity, and are useful for treating HCV infection by
CC inhibiting translation of type I-V HCV RNA. Hepatitis C virus is a
CC positive strand RNA virus, and is the major causative agent of post-
CC transfusion hepatitis. Persistent HCV infection can lead to chronic
CC hepatitis, cirrhosis, and hepatocellular carcinoma
XX
XX Sequence 28 BP; 5 A; 10 C; 5 G; 8 T; 0 U; 0 Other;

Query Match      98.1%; Score 20.6; DB 3; Length 28;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||
Db 6 CCCTGTGAGGAAGTCTGTCT 26

RESULT 18
ADV04753
ID ADV04753 standard; DNA; 28 BP.
XX
AC ADV04753;
XX

```

```

DT 24-FEB-2005 (first entry)
XX
DE Synthetic PCR primer #4.
XX
KW Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.
XX
OS Synthetic.
XX
PN WO2004104198-A1.
XX
PD 02-DEC-2004.
XX
XX 25-NOV-2003; 2003WO-JP015038.
PF
XX
PR 26-MAY-2003; 2003JP-00148242.
PR 19-SEP-2003; 2003JP-00329115.
XX
XX (TORA ) TORAY IND INC.
PA (TORM-) TOKYO METROPOLITAN ORG MEDICAL RES.
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Wakita T, Kato T, Date T;
XX
XX WPI; 2005-013292/01.
XX
XX Novel replicon RNA, having sequence of 5' and 3' untranslated region and
PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic
PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C
PT virus infection.
XX
PS Example 5; SEQ ID NO 19; 197pp; Japanese.
XX
XX The invention relates to replicon RNA from genotype 2a of hepatitis C
CC virus comprising a 5' untranslated region, a base sequence encoding NS3
CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a
CC 3' untranslated region. The invention also relates to a cell capable of
CC reproducing the replicon involving transducing the replicon RNA to a
CC cell, a method of producing a hepatitis C virus protein, a method of
CC screening a substance that promotes or suppresses the reproduction of
CC hepatitis C virus, involving culturing the replicon reproducing cell in
CC the presence of a test substance, and detecting the reproduction of
CC replicon RNA in the culture. Virucide. The replicon RNA is useful for
CC producing a replicon reproduction cell and for increasing the
CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype
CC 2a. The cell and the replicon RNA are useful for producing a therapeutic
CC agent or a diagnostic agent for hepatitis C virus infection, for
CC producing a vaccine against hepatitis C virus infection and for screening
CC a substance that promotes or suppresses the reproduction of hepatitis C
CC virus. This sequence represents a PCR primer used in the scope of the
XX invention.
XX
XX Sequence 28 BP; 5 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

Query Match      98.1%; Score 20.6; DB 14; Length 28;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||
Db 2 CCCTGTGAGGAAGTCTGTCT 22

RESULT 19
ADV04766
ID ADV04766 standard; DNA; 28 BP.
XX
AC ADV04766;
XX
XX 24-FEB-2005 (first entry)
DT
XX
DE Synthetic PCR primer #17.
XX
XX Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.
XX

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OS Synthetic.


```
OS Synthetic.
OS Hepatitis C virus.
PN WO9804745-A1.
XX
XX
PD
XX
XX 05-FEB-1998.
XX
PF 30-JUL-1997; 97WO-US013390.
XX
XX 31-JUL-1996; 96US-00690495.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Zhang DY, Brandwein M;
XX WPI; 1998-159153/14.
XX
XX Detection of target nucleic acids in samples - using capture and
PT amplification probes, paramagnetic particles and ligation to form a
PT nucleotide sequence which can be detected.
XX
XX Example 4; Page 62; 136pp; English.
XX
XX The present sequence represents a probe used in an example of the present
XX invention for the detection of HCV RNA in a sample. The present invention
XX describes methods for: (A) detecting a target nucleic acid (NA) in a
XX sample; (B) in situ detection of a target NA in a sample; (C) detecting
XX an antigen in a sample; and (D) detecting an antibody in a sample. The
XX methods can be used for the rapid automated detection and monitoring of
XX pathogenic organisms, as well as the detection of abnormal genes in an
XX individual. The methods allow for isolation, amplification and detection
XX of NA sequences corresponding to the target NA to be carried out in the
XX same receptacle, e.g. tube or micro-well plate. The method also allows
XX for standardisation of conditions, because only a pair of generic
XX amplification probes may be utilised in the present method for detecting
XX a variety of target NAs, thus allowing efficient multiplex amplification.
XX The method also allows the direct detection of RNA by probe amplification
XX without the need for DNA template production. The amplification probes,
XX which may be covalently joined end to end, form a contiguous ligated
XX amplification sequence. The assembly of the amplifiable DNA by ligation
XX increase specificity, and makes possible the detection of a single
XX mutation in a target
XX
XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 98.1%; Score 20.6; DB 2; Length 45;
XX Best Local Similarity 95.2%; Pred. No. 3.5;
XX Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 31 CCCTGTGAGGAAGTCTGTCT 11
XX
RESULT 22
AAV05026/c
ID AAV05026 standard; DNA; 45 BP.
XX
XX AAV05026;
AC
XX
XX 25-JUN-1998 (first entry)
DT
XX
XX Probe PA of the specification.
DE
XX
XX Human immunodeficiency virus type 1; separation; microbe; PCR primer;
KW amplify; ss.
XX
XX Synthetic.
XX
XX JP10001493-A.
XX
XX 06-JAN-1998.
XX
XX
```

```
PF 24-FEB-1997; 97JP-00039135.
XX
XX 26-FEB-1996; 96EP-00102812.
XX
XX (JAPS ) NIPPON GOSEI GOMU KK.
XX
XX WPI; 1998-114803/11.
XX
XX Separation of nucleic acids from sample - comprises isolation of
PT microbial genetic material, probing and recovering target molecule.
XX
XX Disclosure; Page 8; 12pp; Japanese.
XX
XX PCR primers AAV05022-25. appear in the specification. They are used to
XX amplify part of the Human immunodeficiency virus type I nucleic acid. The
XX specification describes a method for the separation of a target microbial
XX nucleic acid from a biological fluid sample. The method comprises
XX isolating a liquid fraction comprising a microorganism from a sample,
XX isolating the microbial nucleic acid from the liquid fraction, combining
XX a probe with the nucleic acid and recovering the probed nucleic acid. A
XX protein denaturing agent is added between any of the steps
XX
XX Sequence 45 BP; 10 A; 16 C; 11 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 98.1%; Score 20.6; DB 2; Length 45;
XX Best Local Similarity 95.2%; Pred. No. 3.5;
XX Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 25 CCCTGTGAGGAAGTCTGTCT 5
XX
RESULT 23
AAV22769/c
ID AAV22769 standard; DNA; 45 BP.
XX
XX AAV22769;
AC
XX
XX 27-AUG-2003 (revised)
DT
XX
XX 22-JUL-1998 (first entry)
DT
XX
XX Capture/Amp-probe-1 (HCV A) for detecting Hepatitis C virus 5' UTR RNA.
DE
XX
XX Probe; Capture/Amp-probe-1 (HCV A); automated detection; Mycobacteria;
KW nucleic acid; monitoring; pathogenic organism; abnormal gene; ss.
XX
XX Synthetic.
OS Hepatitis C virus.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /+tag= a
FT /note= "biotinylated"
XX
XX WO9804746-A1.
PN
XX
XX 05-FEB-1998.
PD
XX
XX 30-JUL-1997; 97WO-US013391.
PF
XX
XX 31-JUL-1996; 96US-00690494.
PR
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
PA
XX
XX Zhang DY, Brandwein M, Heuh TCH;
PI
XX
XX WPI; 1998-159154/14.
XX
XX Detection of target nucleic acids in samples - using capture and
PT amplification probes, paramagnetic particles and ligation to form a
PT nucleotide sequence which is amplified.
XX
XX
```

PS Example 5; Page 59; 142pp; English.

XX The present sequence represents a probe, designated Capture/Amp-probe-1 (HCV A), used for detecting the 5' untranslated region (5' UTR) of Hepatitis C virus RNA. Nucleotides 5-45 at the 3' end of the probe are complementary to a portion of the 5'UTR of the HCV genome. The probe is used to exemplify the method of the invention, which describes the detection of a target nucleic acid in a sample. The method comprises contacting the target nucleic acid with oligonucleotide probes in the presence of paramagnetic particles coated with a ligand binding moiety. Each capture/amplification probe has a ligand bound to its non-complementary sequence that is capable of binding to and forming an affinity pair with the ligand binding moiety coated onto the paramagnetic particles. The oligonucleotide probes also comprise a probe that can be circularised, by having the 3' and 5' ends ligated together. The circularised probe is amplified with a DNA polymerase having strand displacement activity under conditions whereby an extension primer is extended around the circle for multiple revolutions to form a single stranded DNA of repeating units complementary to the sequence of the circular probe, and multiple copies of a second extension primer hybridise to complementary regions of the single stranded DNA and are extended by the DNA polymerase to provide extension products. The extension products of the second extension primer displace downstream copies of the second extension primer and corresponding extension products to provide displaced single strands to which multiple copies of the first extension primer bind and are extended by the DNA polymerase. The amplified DNA is detected. The method can be used for the rapid automated detection and monitoring of pathogenic organisms as well as the detection of abnormal genes in an individual. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

SQ Query Match 98.1%; Score 20.6; DB 2; Length 45;
Best Local Similarity 95.2%; Pred. No. 3.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 24
ABK86838/c
ID ABK86838 standard; DNA; 45 BP.
XX
AC ABK86838;
XX
XX 24-SEP-2002 (first entry)
XX Hepatitis C A virus 5' UTR capture/Amp probe-1.
DE
DE Hepatitis C; RNA detection; ss; probe; nucleic acid detection;
KW infectious disease.
KW
XX Hepatitis C virus.
OS
XX WO200244339-A2.
PN
XX
XX 06-JUN-2002.
XX
XX 03-DEC-2001; 2001WO-US045822.
XX
XX 01-DEC-2000; 2000US-00728265.
XX (ZHAN/) ZHANG D Y.
PA (BRAN/) BRANDWEIN M.
PA (HSUI/) HSUIH T C H.
XX
XX Zhang DY, Brandwein M, Hsuih TCH;
PI
XX WPI; 2002-508508/54.
DR
XX

PT Detecting a target nucleic acid by a ramification-extension amplification method, involves carrying out the steps of capturing, carrying out ligand-dependent amplification and detection of the target nucleic acid.

PT

XX Example 5; Page 79; 160pp; English.

XX This invention relates to a novel method for detecting target nucleic acid using a Capture/Amplification (C/A) probe and an amplification probe (A-probe), where C/A probe contains generic sequences and sequences complementary to target nucleic acid sequence, and also contains a ligand bound to the non-complementary sequence of probe; the ligand is capable of forming an affinity pair with a ligand binding moiety coated on a matrix. The method of the invention may be used for detecting a target nucleic acid in sample. Preferably, the method is useful for detecting and quantitating nucleic acids from pathogenic microorganisms, from samples from patients with infectious diseases. The method allows for rapid, sensitive and standardised detection and quantification of nucleic acids from pathogenic microorganisms from samples from patients with infectious diseases. The method simplifies the target nucleic acid isolation procedure, which can be performed in microtubes, microchips or micro-well plates, if desired. The method also allows the direct detection of RNA by probe amplification without the need for DNA template production. The assembly of the amplifiable DNA by ligation increases specificity, and makes possible the detection of a single mutation in a target. The method can be easily automated. The present sequence represents the hepatitis C virus capture/ Amp probe-1 used to detect Hepatitis C RNA in an example of the method of the invention

XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

SQ Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 3.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 25
AAD56315/c
ID AAD56315 standard; DNA; 45 BP.
XX
AC AAD56315;
XX
XX 07-AUG-2003 (first entry)
XX Hepatitis C virus (HCV) RNA specific probe, Capture/Amp-probe-1 (HCV A).
DE
DE Detection; pathogen; tumour; Hepatitis C virus; HCV; PCR; probe; ss.
KW
XX Hepatitis C virus.
OS
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Biotinylated"
XX
XX WO2003033722-A2.
XX
XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032754.
XX
XX 15-OCT-2001; 2001US-00978261.
XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Zhang DY;
PI
XX WPI; 2003-393537/37.
DR
XX

PT Detecting target nucleic acids in a sample by analyzing differential mRNA
PT expression, useful for carrying out clinical assays for the detection of
PT infectious pathogenic agents or microorganisms and abnormal genes in an
PT individual.

XX Example 5; Page 78; 166pp; English.

XX The invention relates to methods and kits for rapid automated detection
CC of infectious pathogenic agents and normal and abnormal genes. It also
CC relates to a method for detecting target nucleic acids in a sample by
CC analysing differential mRNA expression. The methods and compositions are
CC useful for carrying out clinical assays for the rapid, automated
CC detection of infectious pathogenic agents or microorganisms, as well as
CC to detect abnormal genes, like in tumour conditions, in an individual.
CC The present sequence is a probe used to detect Hepatitis C virus (HCV)
CC RNA. This sequence is used to illustrate the method of the invention

XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 8; Length 45;

Best Local Similarity 95.2%; Pred. No. 3.5;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21

DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 26

ADQ74915/c

ID ADQ74915 standard; DNA; 45 BP.

AC ADQ74915;

DT 07-OCT-2004 (first entry)

DE HCV Capture/Amp probe 1 (HCV-A).

XX Ligation dependent PCR; LD PCR; ss; probe; capture/amplification probe;

KW polymerase chain reaction; strand displacement amplification;

KW transcription mediated amplification;

KW ramification-extension amplification method; RAM; primer extension;

KW differential mRNA expression; genetic variation; genetic disease;

KW neoplasm; infectious agent; HCV.

XX Hepatitis C virus.

OS Synthetic.

XX US2004137484-A1.

XX 15-JUL-2004.

PF 21-NOV-2003; 2003US-00719480.

XX 15-OCT-2001; 2001US-00978261.

PR 15-OCT-2002; 2002WO-US032745.

XX (ZHAN/) ZHANG D Y.

PA (ZHAN/) ZHANG W.

PA (YIJU/) YI J.

XX Zhang DY, Zhang W, Yi J;

XX WPI; 2004-533357/51.

XX Detecting target nucleic acid in sample, by contacting target nucleic
PT acid with circular oligonucleotide probe, adding specific primer pairs,
PT signal moiety, DNA polymerase, and amplifying circular oligonucleotide
PT probe.

XX Example 5; SEQ ID NO 22: 77pp; English.

PS The invention relates to detecting (M1) a target nucleic acid in a

CC

CC sample, involving contacting the target nucleic acid with a circular
CC oligonucleotide probe under conditions that allow hybridisation between
CC complementary sequences in the target nucleic acid and the circular
CC oligonucleotide probe, adding at least one forward primer comprising a
CC sequence complementary to a portion of the circular oligonucleotide
CC probe, adding an oligonucleotide primer pair comprising a first primer
CC and a second primer where the first primer of the pair comprises a first
CC sequence that is substantially identical to a portion of the circular
CC oligonucleotide probe, a second sequence that is complementary to the
CC second primer of the pair, and a signal generating moiety, the second
CC primer of the pair comprises a sequence that is complementary to the
CC first primer and a moiety capable of quenching, masking or inhibiting the
CC activity of the signal generating moiety, and when the first primer and
CC the second primer are bound to one another, the signal is inhibited,
CC adding at least one reverse primer comprising a sequence that is
CC substantially identical to a portion of the circular oligonucleotide
CC probe, adding a DNA polymerase, and amplifying the circular
CC oligonucleotide probe and separating the signal generating moiety and the
CC quenching, masking or inhibitory moiety to generate a signal, where
CC detection of signal indicates the presence of the target nucleic acid in
CC the sample. Also included are a kit for (M1), and amplifying (M2) a
CC circular nucleic acid sequence. In (M1), the circular oligonucleotide
CC probe is formed by ligating the 3' and 5' ends of linear oligonucleotide
CC probe, comprising 3' and 5' ends regions complementary to adjacent
CC sequences in the target nucleic acid under conditions that allow
CC hybridisation between complementary sequences in the target nucleic acid
CC and the linear oligonucleotide probe. The circular probe is amplified
CC using an amplification method chosen from polymerase chain reaction,
CC strand displacement amplification, transcription mediated amplification,
CC ramification-extension amplification method (RAM) and primer extension.
CC (M1) is useful for detecting a target nucleic acid in a sample. (M2) is
CC useful for amplification of genomic DNA and total mRNAs expressed in
CC cells and for analysing differential mRNA expression. (M1) is useful for
CC detecting genetic variations in nucleic acids in sample from patients
CC with genetic diseases or neoplasia. The DNA and/or mRNA amplified by (M2)
CC is used in techniques developed for detection of infectious agents, and
CC detection of normal and abnormal genes. (M1) is used in clinical assays
CC to detect and monitor pathogenic microorganisms in a test sample, as well
CC as to detect abnormal genes in an individual. (M1) is useful for routine
CC diagnostic testing in a clinical laboratory setting. The present sequence
CC is a capture/amplification probe used to demonstrate the above methods.

XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 12; Length 45;

Best Local Similarity 95.2%; Pred. No. 3.5;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21

DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 27

AEB17467/c

ID AEB17467 standard; DNA; 45 BP.

AC AEB17467;

XX 08-SEP-2005 (first entry)

XX HCV 5'UTR RNA probe, Capture/Amp-probe-1 (HCV A) SEQ ID No:22.

XX DNA detection; RNA detection; hybridization; 5'UTR; probe; ss.

XX Hepatitis C virus.

OS Synthetic.

XX WO2005061722-A1.

XX 07-JUL-2005.

XX 21-NOV-2003; 2003WO-US037199.

XX PR 21-NOV-2003; 2003WO-US037199.
XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX PA (ZHAN/) ZHANG D Y.
XX PA (ZHAN/) ZHANG W.
XX PA (YIUJ/) YI J.
XX PI Zhang DY, Zhang W, Yi J;
XX PI WPI; 2005-488654/49.
XX PT Detecting target nucleic acid for detecting pathogenic agents, by
XX PT contacting target nucleic acid with circular oligonucleotide probe and
XX PT amplifying circular oligonucleotide probe to generate signal, indicating
XX PT presence of nucleic acid.
XX PS Example 5; SEQ ID NO 22; 145pp; English.
XX CC The invention relates to a method of detecting a target nucleic acid in a
XX CC sample. The method comprises: (a) contacting the target nucleic acid with
XX CC a circular oligonucleotide probe that allows hybridization between
XX CC complementary sequences in the target nucleic acid and the circular
XX CC oligonucleotide probe; (b) adding at least one forward primer comprising
XX CC a sequence complementary to a portion of the circular oligonucleotide
XX CC probe; (c) adding an oligonucleotide primer pair comprising a first
XX CC primer and a second primer, where the first primer of the pair comprises
XX CC a first sequence that is substantially identical to a portion of the
XX CC circular oligonucleotide probe, a second sequence that is complementary
XX CC to the second primer of the pair, and a signal generating moiety; the
XX CC second primer of the pair comprises a sequence that is complementary to
XX CC the first primer and a moiety capable of quenching, masking, or
XX CC inhibiting the activity of the signal generating moiety when located
XX CC adjacent to, or in close proximity to, the signal generating moiety; and
XX CC when the first primer and the second primer are bound to one another, the
XX CC signal is inhibited; (d) adding at least one reverse primer comprising a
XX CC sequence that is substantially identical to a portion of the circular
XX CC oligonucleotide probe; (e) adding a DNA polymerase; and (f) amplifying
XX CC the circular oligonucleotide probe thus separating the signal generating
XX CC moiety and the quenching, masking, or inhibitory moiety to generate a
XX CC signal, where detection indicates the presence of the target nucleic acid
XX CC in the sample. Also described are various kits for detecting a target
XX CC nucleic acid. The method and kits of the invention are useful for
XX CC detecting a target nucleic acid in a sample. They are also useful for the
XX CC detection of pathogenic agents, and normal and abnormal genes. This
XX CC sequence represents a probe for the 5'UTR region of Hepatitis C virus
XX CC (HCV) RNA.
XX SQ Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 14; Length 45;
Best Local Similarity 95.2%; Pred. No. 3.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 31 CCCTGTGAGGAAGTCTGTCT 11
RESULT 28
AEB54511/c
ID AEB54511 standard; DNA; 45 BP.
XX AC AEB54511;
XX DT 22-SEP-2005 (first entry)
XX DE HCV detecting probe Capture/Amp-probe-1 SEQ ID NO 22.
XX KW ss; probe; DNA detection; screening.
XX OS Hepatitis C virus.
XX FT

PN WO2005060725-A2.
XX PD 07-JUL-2005.
XX PF 10-MAR-2004; 2004WO-US007237.
XX PR 21-NOV-2003; 2003US-00791480.
XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX PA (ZHAN/) ZHANG D Y.
XX PA (ZHAN/) ZHANG W.
XX PA (YIUJ/) YI J.
XX PI Zhang DY, Zhang W, Yi J;
XX PI WPI; 2005-554597/56.
XX PT Detecting target nucleic acid, by contacting target with specific
XX PT circular probe, forward primer having sequence complementary to probe,
XX PT primer pair, reverse primer having sequence identity to probe and
XX PT polymerase, and amplifying probe.
XX PS Example 5; SEQ ID NO 22; 171pp; English.
XX CC This invention describes a novel method of detecting target nucleic acid
XX CC comprising contacting the target with circular oligonucleotide probe,
XX CC adding forward primer having sequence complementary to the probe, adding
XX CC oligonucleotide primer pair, where when the first and second primers are
XX CC bound to one another, the signal is inhibited, adding reverse primer
XX CC having sequence identical to portion of the probe, adding a DNA
XX CC polymerase and amplifying the probe. The detection methods of the
XX CC invention are useful for 1) amplifying and detecting genomic DNA and
XX CC total mRNAs and for analyzing differential mRNA expression within
XX CC different cells; 2) for screening a large number of tumor cells at
XX CC different stages of tumorigenesis and identification of important genes
XX CC that are closely related to tumorigenesis; 3) for detecting and
XX CC quantifying nucleic acids from infectious pathogenic agents, and normal
XX CC and abnormal genes; 4) for generating increased quantities of DNA and/or
XX CC mRNA from small number of cells; 5) for rapid, highly sensitive, accurate
XX CC and automated detection of infectious pathogenic agents and normal and
XX CC abnormal genes. This sequence represents a probe used to detect Hepatitis
XX CC C virus infection.
XX SQ Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 14; Length 45;
Best Local Similarity 95.2%; Pred. No. 3.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 31 CCCTGTGAGGAAGTCTGTCT 11
RESULT 29
AAQ53262
ID AAQ53262 standard; RNA; 51 BP.
XX AC AAQ53262;
XX DT 25-MAR-2003 (revised)
XX DT 13-JUN-1994 (first entry)
XX DE Hepatitis C virus probe complex.
XX KW Detection; HCV; 6:2 probe design.
XX OS Hepatitis C virus.
XX FT Key modified_base 1 Location/Qualifiers
XX FT /*tag= a
XX FT /note= "fluorescein labelled"

```
FT modified_base 51
FT FT /*tag= b
FT /note= "Biotin labelled"
PN W09324656-A1.
XX 09-DEC-1993.
PD
XX 24-MAY-1993; 93WO-US0004863.
PF
XX 29-MAY-1992; 92US-00891543.
PR
XX (ABBO ) ABBOTT LAB.
PA
XX Marshall RL, Carrino JJ, Sustachek JC;
XX WPI; 1993-405844/50.
XX
XX Amplifying known RNA target for use in diagnosis of HIV and HCV infection
PT - by treating sample RNA with oligo-nucleotide probe, extending probe by
PT reverse transcription of target, dissociating probe from target,
PT hybridising 2nd probe with 1st, etc.
XX
XX Example 2; Page 16; 49pp; English.
XX
XX The sequence is that of a complex formed by probes (AAQ53237-Q53240) used
CC in the detection of hepatitis C virus (HCV) using a 6:2 probe design.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 51 BP; 14 A; 16 C; 10 G; 11 T; 0 U; 0 Other;
SQ
Query Match 98.1%; Score 20.6; DB 2; Length 51;
Best Local Similarity 95.2%; Pred. No. 3.6;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 16 CCCTGTGAGGAACACTACTGTCT 36
RESULT 30
AAZ57776/C
ID AAZ57776 standard; DNA; 67 BP.
XX
XX AAZ57776;
AC
XX 05-APR-2000 (first entry)
DT
XX Hepatitis C virus antisense inhibitor oligonucleotide #42.
DE
XX Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
XX Hepatitis C virus.
OS
XX US6001990-A.
PN
XX 14-DEC-1999.
PD
XX 07-JUN-1995; 95US-00474700.
PF
XX 10-MAY-1994; 94US-00240382.
PR
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX Moradpour D, Wands JR, Wakita T;
PI
XX WPI; 2000-104900/09.
DR
XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections.
XX
XX Claim 31; Col 33; 31pp; English.
PS
```

```
XX This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
XX
XX Sequence 67 BP; 13 A; 15 C; 25 G; 14 T; 0 U; 0 Other;
SQ
Query Match 98.1%; Score 20.6; DB 3; Length 67;
Best Local Similarity 95.2%; Pred. No. 3.7;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 25 CCCTGTGAGGAACACTACTGTCT 5
RESULT 31
ADW39164
ID ADW39164 standard; RNA; 70 BP.
XX
XX ADW39164;
AC
XX 24-MAR-2005 (first entry)
DT
XX Novel nucleic acid amplification method-related oligonucleotide SeqID1.
DE
XX DNA detection; RNA detection; ss.
KW
XX Unidentified.
OS
XX CN1460722-A.
PN
XX 10-DEC-2003.
PD
XX 19-MAY-2003; 2003CN-00123596.
PF
XX 19-MAY-2003; 2003CN-00123596.
PR
XX (TIAN/) TIAN J.
PA
XX Tian J, Gong Q;
PI
XX WPI; 2004-181274/18.
DR
XX Method for nucleic acid amplification detection, comprises using a line
PT probe and a ring probe and a one-step constant temperature reaction.
PT
XX Example 1; SEQ ID NO 1; 31pp; Chinese.
PS
XX This invention relates to a novel nucleic acid amplification detection
CC method. The invention can implement several operations of nucleic acid
CC hybridization, amplification and detection in the same reaction tube, by
CC only using one kind of DNA polymerase and by means of a one-step constant
CC temperature reaction. The invention is applicable to detection of RNA and
CC DNA. The present sequence is that of an oligonucleotide which was used in
CC the exemplification of the method of the invention.
XX
XX Sequence 70 BP; 17 A; 21 C; 16 G; 0 T; 16 U; 0 Other;
SQ
Query Match 98.1%; Score 20.6; DB 13; Length 70;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 18 CCCUGUGAGGAACUACUGUCU 38
```

RESULT 32
 AAL40115
 ID AAL40115 standard; DNA; 73 BP.
 XX
 AC AAL40115;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Pathogenic microorganism detecting PCR primer SEQ ID No 41.
 XX
 XX Tuberculosis; Mycobacterium; bovis; BCG; africanum; microti; canottii;
 KW monitoring therapy; pathogenic microorganism; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200252043-A1.
 XX
 XX 04-JUL-2002.
 PD
 XX
 XX 26-DEC-2001; 2001WO-JP011422.
 PF
 XX
 PR 26-DEC-2000; 2000JP-00396222.
 PR
 PR 26-DEC-2000; 2000JP-00396321.
 PR
 PR 29-JUN-2001; 2001JP-00199552.
 PR
 PR 13-SEP-2001; 2001JP-00278920.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX
 XX Shimada M, Hino F, Kato I;
 PI
 XX
 XX WPI; 2002-500769/53.
 DR
 XX
 XX Detecting pathogenic microorganisms with oligonucleotide probes and
 PT primers, useful in disease diagnosis and monitoring therapy.
 PT
 XX
 XX Claim 57; Page 97; 106pp; Japanese.
 PS
 XX
 XX The invention relates to a probe containing a 410 or 20 base pair
 CC sequence, given in the specification. It is capable of detecting the
 CC tuberculosis bacterial group including Mycobacterium tuberculosis,
 CC Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti
 CC and/or Mycobacterium canottii. The method is useful in disease diagnosis
 CC and monitoring therapy. This polynucleotide sequence represents a PCR
 CC primer relating to the detection of pathogenic microorganisms of the
 CC invention
 XX
 SQ Sequence 73 BP; 18 A; 23 C; 15 G; 17 T; 0 U; 0 Other;
 KW Virucide; Cytostatic; p110 subunit;
 KW eukaryotic translation initiation factor eIF3; region II;
 KW internal ribosome entry site; IRES; aminoglycoside; viral infection;
 KW hepatitis C infection; swine fever; bovine diarrhoea; viral cancer; ds.
 XX
 XX Hepatitis C virus.
 OS
 XX
 XX FR2848572-A1.
 PN
 XX
 XX 18-JUN-2004.
 PD
 XX
 XX 12-DEC-2002; 2002FR-00015718.
 PF
 XX
 XX 12-DEC-2002; 2002FR-00015718.
 PR
 XX
 XX (UYFO-) UNIV FOURIER JOSEPH.
 PA
 XX
 XX Balakireva L;
 PI
 XX
 XX WPI; 2004-452919/43.
 DR
 XX
 XX In vitro screening for antiviral agents, from ability to inhibit complex
 PT formation between the p110 subunit of translation initiation factor eIF3
 PT and region II of the viral internal ribosome binding site.
 PT

PN CN1460722-A.
 XX
 PD 10-DEC-2003.
 XX
 XX 19-MAY-2003; 2003CN-00123596.
 PF
 XX
 XX 19-MAY-2003; 2003CN-00123596.
 PR
 XX
 XX (TIAN/) TIAN J.
 PA
 XX
 XX Tian J, Gong Q;
 PI
 XX
 XX WPI; 2004-181274/18.
 DR
 XX
 XX Method for nucleic acid amplification detection, comprises using a line
 PT probe and a ring probe and a one-step constant temperature reaction.
 PT
 XX
 XX Example 1; SEQ ID NO 3; 31pp; Chinese.
 PS
 XX
 XX This invention relates to a novel nucleic acid amplification detection
 CC method. The invention can implement several operations of nucleic acid
 CC hybridization, amplification and detection in the same reaction tube, by
 CC only using one kind of DNA polymerase and by means of a one-step constant
 CC temperature reaction. The invention is applicable to detection of RNA and
 CC DNA. The present sequence is that of an oligonucleotide which was used in
 CC the exemplification of the method of the invention.
 XX
 XX Sequence 79 BP; 26 A; 18 C; 18 G; 17 T; 0 U; 0 Other;
 SQ
 Query Match 98.1%; Score 20.6; DB 13; Length 79;
 Best Local Similarity 95.2%; Pred. No. 3.8;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTGTGAGGAAGTCTGTCT 21
 Db 41 CCCTGTGAGGAAGTCTGTCT 21
 RESULT 34
 ADP20411
 ID ADP20411 standard; DNA; 80 BP.
 AC
 AC ADP20411;
 XX
 XX 09-SEP-2004 (first entry)
 DT
 XX
 XX Hepatitis C virus IRES, region II sequence, SEQ ID 2.
 DE
 XX
 KW Virucide; Cytostatic; p110 subunit;
 KW eukaryotic translation initiation factor eIF3; region II;
 KW internal ribosome entry site; IRES; aminoglycoside; viral infection;
 KW hepatitis C infection; swine fever; bovine diarrhoea; viral cancer; ds.
 XX
 XX Hepatitis C virus.
 OS
 XX
 XX FR2848572-A1.
 PN
 XX
 XX 18-JUN-2004.
 PD
 XX
 XX 12-DEC-2002; 2002FR-00015718.
 PF
 XX
 XX 12-DEC-2002; 2002FR-00015718.
 PR
 XX
 XX (UYFO-) UNIV FOURIER JOSEPH.
 PA
 XX
 XX Balakireva L;
 PI
 XX
 XX WPI; 2004-452919/43.
 DR
 XX
 XX In vitro screening for antiviral agents, from ability to inhibit complex
 PT formation between the p110 subunit of translation initiation factor eIF3
 PT and region II of the viral internal ribosome binding site.
 PT

XX PS Claim 1; SEQ ID NO 2; 45pp; French.
XX CC
CC The present invention relates to an in vitro method of screening for
CC compounds (A) that inhibit the formation of a complex between the p110
CC subunit (ADP20413) of the eukaryotic translation initiation factor eIF3
CC and region II of the internal ribosome entry site (IRES; ADP20411) of
CC hepatitis C virus (HCV). Preferably the p110 recognition motif (ADP20414)
CC and the region II consensus sequence (ADP20412), or fragment of it
CC containing at least 8 consecutive nucleotides, are used. (A) is
CC especially an aminoglycoside, specifically tobramycin or an
CC oligonucleotide antisense to consensus sequence ADP20412, or parts of it.
CC (A) are used for treating infection by hepatitis C, swine fever and
CC bovine diarrhoea viruses, also for treating viral or non-viral diseases
CC which involve proteins synthesis of which is initiated from an IRES, e.g.
CC cancer.
XX CC
SQ Sequence 80 BP; 17 A; 21 C; 22 G; 20 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 12; Length 80;
Best Local Similarity 95.2%; Pred. No. 3.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTCTCTCT 21
Db 4 CCCTGTGAGGAACCTCTCTCT 24

RESULT 35
AAD33033
ID AAD33033 standard; DNA; 85 BP.
XX AC
XX AD33033;
XX DT 01-JUL-2002 (first entry)
XX DE HCV-S1 overlapping cDNA region amplifying sense PCR primer, H28.
XX KW Nucleic acid construct; expression cassette; non-coding region; NCR;
XX KW untranslated region; UTR; anti-viral drug; drug resistance; primer; PCR;
XX KW HCV-S1; Hepatitis C virus; ss.
XX OS Hepatitis C virus.
XX PN WO200208447-A2.
XX PD 31-JAN-2002.
XX PF 20-JUL-2001; 2001WO-IL000669.
XX PR 24-JUL-2000; 2000US-0220248P.
XX PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX PA (EHRLL/) EHRLLICH G.
XX PI Tan YH, Lim SP, Lim SG, Hong WJ;
XX DR WPI; 2002-280605/32.
XX PT Novel nucleic acid construct useful for detecting the presence of RNA
XX virus, comprises an expression cassette and a promoter operably linked to
XX expression cassette for minus strand RNA transcription of the cassette.
XX PS Example 1; Page 24; 81pp; English.
XX CC
CC The invention relates to nucleic acid construct which comprises an
CC expression cassette including a first polynucleotide region including a
CC 5' non-coding region (NCR) sequence of an RNA virus and at least an N-
CC terminal portion of a coding sequence of RNA virus, a second
CC polynucleotide region including a 3' untranslated region (UTR) sequence
CC of the RNA virus and at least a C-terminal portion of a coding sequence
CC of the virus and a third polynucleotide region encoding a reporter
CC molecule, flanked by first and second polynucleotide regions; and a

CC promoter sequence being operatively linked to expression cassette in a
CC manner so as to enable a transcription of a minus strand RNA molecule
CC from the expression cassette. Nucleic acid construct of the invention is
CC useful for detecting the presence of an RNA virus in a cell. It is also
CC useful for screening anti-viral drugs and determining drug resistance of
CC an RNA virus. The present sequence is a PCR primer used to amplify the
CC overlapping cDNA regions of the genome of Hepatitis C virus (HCV) isolate
CC HCV-S1. Note: This sequence is stated to be same as that shown as SEQ ID
CC NO:26 in the sequence listing of the specification, however this sequence
XX has 2 additional bases at its 3' end
XX
SQ Sequence 85 BP; 20 A; 30 C; 20 G; 15 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 6; Length 85;
Best Local Similarity 95.2%; Pred. No. 3.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTCTCTCT 21
Db 43 CCCTGTGAGGAACCTCTCTCT 63

RESULT 36
ADW39165
ID ADW39165 standard; DNA; 95 BP.
XX AC
XX ADW39165;
XX DT 24-MAR-2005 (first entry)
XX DE Novel nucleic acid amplification method-related oligonucleotide SeqID2.
XX KW DNA detection; RNA detection; ss.
XX OS Unidentified.
XX PN CN1460722-A.
XX PD 10-DEC-2003.
XX PF 19-MAY-2003; 2003CN-00123596.
XX PR 19-MAY-2003; 2003CN-00123596.
XX PA (TIAN/) TIAN J.
XX PI Tian J, Gong Q;
XX DR WPI; 2004-181274/18.
XX PT Method for nucleic acid amplification detection, comprises using a line
XX probe and a ring probe and a one-step constant temperature reaction.
XX PS Example 1; SEQ ID NO 2; 31pp; Chinese.
XX
XX This invention relates to a novel nucleic acid amplification detection
XX method. The invention can implement several operations of nucleic acid
XX hybridization, amplification and detection in the same reaction tube, by
XX only using one kind of DNA polymerase and by means of a one-step constant
XX temperature reaction. The invention is applicable to detection of RNA and
XX DNA. The present sequence is that of an oligonucleotide which was used in
XX the exemplification of the method of the invention.
XX
SQ Sequence 95 BP; 27 A; 26 C; 20 G; 22 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 13; Length 95;
Best Local Similarity 95.2%; Pred. No. 3.9;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTCTCTCT 21
Db 43 CCCTGTGAGGAACCTCTCTCT 63

RESULT 37
 ID ADR05701
 AD ADR05701 standard; RNA; 103 BP.
 XX
 AC ADR05701;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Hepatitis C virus UTR domain I1ab RNA fragment SEQ ID NO:14.
 XX
 KW screening; identification; RNA regulatory element; reporter mRNA;
 KW medicine; gene expression modulation; Hepatitis C virus; HCV;
 KW untranslated region; UTR; gene; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2004067728-A2.
 XX
 PD 12-AUG-2004.
 XX
 PF 09-JAN-2004; 2004WO-US000423.
 XX
 PR 17-JAN-2003; 2003US-0441028P.
 XX
 PA (PTCT-) PTC THERAPEUTICS.
 XX
 PI Pellegrini MC, Trotta CR, Huq SI;
 XX
 DR WPI; 2004-581000/56.
 XX
 Screening for and/or identifying (non-cell based) an RNA regulatory
 element comprises combining a translation extract, an RNA test sequence,
 PT and a reporter mRNA under conditions suitable for translation of the
 PT reporter mRNA.
 XX
 PS Example 2; SEQ ID NO 14; 87pp; English.
 XX
 The present invention describes a non-cell based method of screening for
 and/or identifying an RNA regulatory element. The method comprises
 CC combining a translation extract, an RNA test sequence, and a reporter
 CC mRNA under conditions suitable for translation of the reporter mRNA, and
 CC measuring the effect of the test sequence on the translation of the
 CC reporter mRNA, where a test sequence that modifies the translation of the
 CC reporter mRNA includes an RNA regulatory element. Also described: (1) a
 CC non-cell based method of screening for and/or identifying at least one
 CC test compound which modulates the ability of an RJSTA sequence to
 CC regulate translation of a reporter mRNA; (2) an in vitro translation
 CC system for screening for and/or identifying a test compound, which
 CC modulates the ability of an RNA regulatory sequence to regulate
 CC translation of a reporter mRNA; (3) screening for and/or identifying a
 CC test compound, which modulates the ability of an RNA regulatory sequence
 CC to regulate translation of a reporter mRNA; (4) an in vitro translation
 CC system for screening for and/or identifying a test compound capable of
 CC reversing the inhibition of translation mediated by an RNA regulatory
 CC sequence; (4) screening for and/or identifying a test compound, which
 CC reverses inhibition of translation; and (5) a test compound identified
 CC according to the method described above. The methods and systems are
 CC useful for screening for and/or identifying an RNA regulatory element.
 CC The test compound is useful for the manufacture of a medicine for
 CC modulating the expression of a gene comprising the RNA sequence or of the
 CC protein expressed from a construct engineered to include the RNA
 CC sequence. The expression of the gene is aberrant in a disease state that
 CC causes the survival and/or progression of a pathogenic organism. The
 CC present sequence represents a Hepatitis C virus untranslated region (UTR)
 CC RNA fragment, which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 103 BP; 22 A; 32 C; 27 G; 0 T; 22 U; 0 Other;
 Query Match 98.1%; Score 20.6; DB 13; Length 103;
 Best Local Similarity 66.7%; Pred. No. 3.9;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTWCTCTCT 21
 |||:|:|||||:|:|:|:|:|:|:
 DB 26 CCUGUGAGGAACUACUGUCU 46
 RESULT 38
 ADP87783
 ID ADP87783 standard; cDNA; 110 BP.
 XX
 AC ADP87783;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Hepatitis C virus TEX target cDNA.
 XX
 KW TEX; thermodynamic equilibrium extension of primers; HCV; ss; target.
 XX
 OS Hepatitis C virus.
 XX
 PN US2004115643-A1.
 XX
 PD 17-JUN-2004.
 XX
 PF 12-DEC-2002; 2002US-00318416.
 XX
 PR 12-DEC-2002; 2002US-00318416.
 XX
 PA (LIZA/) LIZARDI P M.
 PA (GRIB/) GRIBANOV O G.
 XX
 PI Lizardi PM, Gribanov OG;
 XX
 DR WPI; 2004-468050/44.
 XX
 Amplifying nucleic acid for detecting nucleic acid, by extension of one
 or more primers using target templates having replication terminating
 PT feature, dissociation of primer from templates to produce multiple
 PT extended primers.
 XX
 PS Disclosure; SEQ ID NO 15; 75pp; English.
 XX
 The invention relates to amplifying (M1) a nucleic acid, involving
 CC contacting one or more extension primers (EP) and target templates (TT)
 CC and incubating under conditions to promote interaction of (EP) and
 CC templates, extension of (EP) using the interacting (TT), and dissociation
 CC of the extended (EP) from (TT), to produce multiple extended (EP) from at
 CC least one (TT), where each (TT) comprise a replication terminating
 CC feature. In (M1), (EP) and target templates are incubated under
 CC isothermal conditions or single set of conditions. The target templates
 CC are nucleic acid sequences of interest. Each of (EP) comprises or
 CC consists of a target complement portion, preferably nucleotides, where
 CC the nucleotides consist of the target complement portion. Each (EP)
 CC further comprises non-target complement portion. The method is known as
 CC TEX (thermodynamic equilibrium extension of primers). The method is
 CC useful for amplifying nucleic acid and for detecting nucleic acid
 CC sequences which involves performing (M1), and detecting one or more of
 CC the extended (EP). In (M1), only those sequences targeted by (EP) are
 CC amplified, thus allowing specific sequences to be targeted for
 CC amplification. Flexibility in the location of replication terminating
 CC feature allows flexibility in targeting sequences. If a targeted sequence
 CC is not present, the sequence will not be amplified. Multiple sequences
 CC can be amplified in the same reaction by targeting multiple sequences
 CC with (EP). Simultaneous amplification and detection is facilitated using
 CC detection probes associated with a substrate. Multiplex detection can be
 CC facilitate by an array of detection probes with different detection
 CC probes at different locations of a substrate. The present sequence is an
 CC HCV (Hepatitis C virus) target sequence detected/amplified by the method
 CC of the invention.
 XX
 SQ Sequence 110 BP; 24 A; 34 C; 28 G; 24 T; 0 U; 0 Other;
 Query Match 98.1%; Score 20.6; DB 12; Length 110;

Best Local Similarity 95.2%; Pred. No. 3.9;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGCT 21
|||||
Db 11 CCCTGTGAGGAAGTCTGCT 31

RESULT 39
ABX03545
ID ABX03545 standard; RNA; 127 BP.
XX
AC ABX03545;
XX
DT 07-JAN-2003 (first entry)
XX
DE Hepatitis C virus 1969 RNA UTR sequence.
XX
KW HCV; hepatitis C virus; NS3 protease; virucide; ss; helicase-Inhibitor;
KW infection.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT stem_loop 5..20
FT /tag= a
FT misc_binding 44..52
FT /tag= b
FT /bound_moiety= "Binds to nucleotides 118..111"
FT misc_binding 56..60
FT /tag= c
FT /bound_moiety= "Binds to nucleotides 107..104"
FT misc_binding 65..70
FT /tag= d
FT /bound_moiety= "Binds to nucleotides 102..97"
FT stem_loop 74..92
FT /tag= e
FT misc_binding 97..102
FT /tag= f
FT /bound_moiety= "Binds to nucleotides 70..65"
FT misc_binding 104..107
FT /tag= g
FT /bound_moiety= "Binds to nucleotides 60..56"
FT misc_binding 111..118
FT /tag= h
FT /bound_moiety= "Binds to nucleotides 52..44"
XX
WO200270752-A1.
XX
PD 12-SEP-2002.
XX
PF 14-FEB-2002; 2002WO-US004916.
XX
PR 14-FEB-2001; 2001US-0269776P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dasgupta A, Banerjee R;
XX
DR WPI; 2002-707103/76.
XX
Assaying a sample containing or suspected of containing hepatitis C virus (HCV) RNA for treating HCV infection comprises measuring the presence of the HCV RNA in the sample that binds to NS3.
XX
Example 2; Fig 3; 66pp; English.
XX
This invention relates to a novel method for assaying a sample containing or suspected of containing hepatitis C virus (HCV) RNA. The method comprises contacting the sample with an NS3 protease protein or its fragment or mutant to form a nucleoprotein complex, and measuring the amount or presence of the HCV RNA in the sample that binds to NS3. The method of the invention may have virucide activity and it may act as a

CC helicase-Inhibitor-NS3. The method of the invention is useful for
CC treating HCV infection. The present sequence represents an RNA sequence
CC representing a mutant form of the HCV 1969 DNA 3' UTR used in the method
CC of the invention
XX
SQ Sequence 127 BP; 26 A; 44 C; 32 G; 0 T; 25 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 6; Length 127;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAAGTCTGCT 21
|||||
Db 43 CCCUGAGGAACUACUGUCU 63

RESULT 40
ADM15169
ID ADM15169 standard; DNA; 131 BP.
XX
AC ADM15169;
XX
DT 07-APR-2005 (first entry)
XX
DE HCV H77C RT-PCR product #3.
XX
KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;
KW infection; drug screening; ss; virucide; gene therapy;
KW reverse transcriptase PCR.
XX
OS Hepatitis C virus; strain H77C.
XX
PN WO2005005625-A2.
XX
PD 20-JAN-2005.
XX
PF 14-JUL-2004; 2004WO-CA001009.
XX
PR 14-JUL-2003; 2003CA-02436104.
XX
PR 06-FEB-2004; 2004CA-02454540.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Sonenberg N, Lopez Lastra M;
XX
DR WPI; 2005-122423/13.
XX
Generating an established cell line that produces hepatitis C virus (HCV)
PT for identifying a compound with anti-HCV activity, comprises transforming
PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
PT virus.
XX
PS Disclosure; Fig 57; 161pp; English.
XX
The invention relates to generating an established cell line that
CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
CC Also included are a method for producing HCV in vitro, an EBV-established
CC B-cell line capable of replicating complete and infectious HCV, a cell-
CC based in vitro replication system for HCV (comprising an EBV-transformed
CC B-cell capable of replicating complete and infectious HCV and a second
CC population having HCV tropism and in which robust HCV replication occurs,
CC so that under appropriate culture conditions the second population can
CC become infected by the infectious HCV produced by the EBV-transformed B-
CC cell), an assay for screening a test agent and selecting an agent that
CC possesses anti-HCV activity and a method for identifying a compound with
CC anti-HCV activity from a library of compounds. The method is useful in
CC generating an established cell line that produces hepatitis C virus (HCV)
CC for identifying a compound with anti-HCV activity. HCV sequence was
CC amplified by reverse transcription from EBV-immortalized cells (derived
CC from patient PBMC samples) and compared to sequence amplified from the
CC infectious strain H77C. The present sequence is a PCR amplicon from the
CC control H77C virus.

Query Match	98.1%;	Score 20.6;	DB 14;	Length 131;
Best Local Similarity	95.2%;	Pred. No. 4;		
Matches	20;	Conservative	1;	Mismatches 0; Gaps 0
QY	1	CCCTGTGAGGAAGTTCGTCT 21		
DB	6	CCCTGTGAGGAAGTTCGTCT 26		
RESULT 42				
ADW15170				
ID	ADW15170	standard; DNA; 131 BP.		
XX	AC	AC		
XX	AC	ADW15170;		
XX	XX	07-APR-2005 (first entry)		
XX	XX	HCV from immortalized cell line 9.2 RT-PCR product #1.		
DE	XX	Cell culture; Hepatitis C virus infection; gastrointestinal disease;		
XX	XX	infection; drug screening; ss; virucide; gene therapy;		
KW	KW	reverse transcriptase PCR.		
KW	KW			
XX	XX	Hepatitis C virus.		
OS	XX			
XX	XX	WO2005005625-A2.		
PN	XX	20-JAN-2005.		
XX	XX			
PD	XX	14-JUL-2004; 2004WO-CR001009.		
XX	XX			
PF	XX	14-JUL-2003; 2003CA-02436104.		
PR	XX	06-FEB-2004; 2004CA-02454540.		
PR	XX	(UYMC-) UNIV MCGILL.		
XX	XX			
PA	XX	Sonenberg N, Lopez Lastra M;		
XX	XX	WPT; 2005-122423/13.		
PI	XX	Generating an established cell line that produces hepatitis C virus (HCV)		
DR	XX	for identifying a compound with anti-HCV activity, comprises transforming		
PT	XX	peripheral blood mononuclear cells that produce HCV with Epstein Barr		
PT	XX	virus.		
PT	XX	Disclosure; Fig 57; 161pp; English.		
XX	XX			
CC	CC	The invention relates to generating an established cell line that		
CC	CC	produces hepatitis C virus (HCV) comprising transforming peripheral blood		
CC	CC	mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).		
CC	CC	Also included are a method for producing HCV in vitro, an EBV-established		
CC	CC	B-cell line capable of replicating complete and infectious HCV, a cell-		
CC	CC	based in vitro replication system for HCV (comprising an EBV-transformed		
CC	CC	B-cell capable of replicating complete and infectious HCV and a second		
CC	CC	population having HCV tropism and in which robust HCV replication occurs,		
CC	CC	so that under appropriate culture conditions the second population can		
CC	CC	become infected by the infectious HCV produced by the EBV-transformed B-		
CC	CC	cell), an assay for screening a test agent and selecting an agent that		
CC	CC	possesses anti-HCV activity and a method for identifying a compound with		
CC	CC	anti-HCV activity from a library of compounds. The method is useful in		
CC	CC	generating an established cell line that produces hepatitis C virus (HCV)		
CC	CC	for identifying a compound with anti-HCV activity. HCV sequence was		
CC	CC	amplified by reverse transcription from EBV-immortalized cell line 9.2		
CC	CC	(derived from patient PBMC samples), passaged through several changes in		
CC	CC	culture medium (designated 9.2a-9.2d cells) and compared to sequence		
CC	CC	amplified from the infectious strain H77C. The present sequence is a PCR		
CC	CC	amplicon from the HCV sequence amplified from EBV cell line 9.2.		

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 43
 ADW15174
 ID ADW15174 standard; DNA; 131 BP.
 XX
 AC ADW15174;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE HCV from immortalized cell line 9.2d RT-PCR product #1.
 XX
 DE HCV from immortalized cell line 9.2b RT-PCR product #1.
 XX
 KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;
 KW infection; drug screening; ss; virucide; gene therapy;
 KW reverse transcriptase PCR.
 XX
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT mutation replace(70,G)
 FT /*tag= a
 FT mutation replace(82,A)
 FT /*tag= b
 XX
 PN WO2005005625-A2.
 XX
 PD 20-JAN-2005.
 XX
 PF 14-JUL-2004; 2004WO-CA001009.
 XX
 PR 14-JUL-2003; 2003CA-02436104.
 PR 06-FEB-2004; 2004CA-02454540.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Sonenberg N, Lopez Lastra M;
 XX
 DR WPI; 2005-122423/13.
 XX
 XX

PT Generating an established cell line that produces hepatitis C virus (HCV)
 PT for identifying a compound with anti-HCV activity, comprises transforming
 PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
 PT virus.
 XX
 PS Disclosure; Fig 57; 161pp; English.
 XX

CC The invention relates to generating an established cell line that
 CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
 CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
 CC Also included are a method for producing HCV in vitro, an EBV-established
 CC B-cell line capable of replicating complete and infectious HCV, a cell-
 CC based in vitro replication system for HCV (comprising an EBV-transformed
 CC B-cell capable of replicating complete and infectious HCV and a second
 CC population having HCV tropism and in which robust HCV replication occurs,
 CC so that under appropriate culture conditions the second population can
 CC become infected by the infectious HCV produced by the EBV-transformed B-
 CC cell), an assay for screening a test agent and selecting an agent that
 CC possesses anti-HCV activity and a method for identifying a compound with
 CC anti-HCV activity from a library of compounds. The method is useful in
 CC generating an established cell line that produces hepatitis C virus (HCV)
 CC for identifying a compound with anti-HCV activity. HCV sequence was
 CC amplified by reverse transcription from EBV-immortalized cell line 9.2
 CC (derived from patient PBMC samples), passaged through several changes in
 CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
 CC amplified from the infectious strain H77C. The present sequence is a PCR
 CC amplicon from the HCV sequence amplified from EBV cell line 9.2d.
 XX
 SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;
 Best Local Similarity 95.2%; Pred. No. 4;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 44
 ADW15172
 ID ADW15172 standard; DNA; 131 BP.
 XX
 AC ADW15172;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE HCV from immortalized cell line 9.2b RT-PCR product #1.
 XX
 DE HCV from immortalized cell line 9.2b RT-PCR product #1.
 XX
 KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;
 KW infection; drug screening; ss; virucide; gene therapy;
 KW reverse transcriptase PCR.
 XX
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT mutation replace(70,G)
 FT /*tag= a
 FT mutation replace(82,A)
 FT /*tag= b
 XX
 PN WO2005005625-A2.
 XX
 PD 20-JAN-2005.
 XX
 PF 14-JUL-2004; 2004WO-CA001009.
 XX
 PR 14-JUL-2003; 2003CA-02436104.
 PR 06-FEB-2004; 2004CA-02454540.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Sonenberg N, Lopez Lastra M;
 XX
 DR WPI; 2005-122423/13.
 XX
 XX

PT Generating an established cell line that produces hepatitis C virus (HCV)
 PT for identifying a compound with anti-HCV activity, comprises transforming
 PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
 PT virus.
 XX
 PS Disclosure; Fig 57; 161pp; English.
 XX

CC The invention relates to generating an established cell line that
 CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
 CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
 CC Also included are a method for producing HCV in vitro, an EBV-established
 CC B-cell line capable of replicating complete and infectious HCV, a cell-
 CC based in vitro replication system for HCV (comprising an EBV-transformed
 CC B-cell capable of replicating complete and infectious HCV and a second
 CC population having HCV tropism and in which robust HCV replication occurs,
 CC so that under appropriate culture conditions the second population can
 CC become infected by the infectious HCV produced by the EBV-transformed B-
 CC cell), an assay for screening a test agent and selecting an agent that
 CC possesses anti-HCV activity and a method for identifying a compound with
 CC anti-HCV activity from a library of compounds. The method is useful in
 CC generating an established cell line that produces hepatitis C virus (HCV)
 CC for identifying a compound with anti-HCV activity. HCV sequence was
 CC amplified by reverse transcription from EBV-immortalized cell line 9.2
 CC (derived from patient PBMC samples), passaged through several changes in
 CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
 CC amplified from the infectious strain H77C. The present sequence is a PCR
 CC amplicon from the HCV sequence amplified from EBV cell line 9.2d.
 XX
 SQ Sequence 131 BP; 27 A; 42 C; 36 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;
 Best Local Similarity 95.2%; Pred. No. 4;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 43
 ADW15174
 ID ADW15174 standard; DNA; 131 BP.
 XX
 AC ADW15174;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE HCV from immortalized cell line 9.2d RT-PCR product #1.
 XX
 DE HCV from immortalized cell line 9.2b RT-PCR product #1.
 XX
 KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;
 KW infection; drug screening; ss; virucide; gene therapy;
 KW reverse transcriptase PCR.
 XX
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT mutation replace(70,G)
 FT /*tag= a
 FT mutation replace(82,A)
 FT /*tag= b
 XX
 PN WO2005005625-A2.
 XX
 PD 20-JAN-2005.
 XX
 PF 14-JUL-2004; 2004WO-CA001009.
 XX
 PR 14-JUL-2003; 2003CA-02436104.
 PR 06-FEB-2004; 2004CA-02454540.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Sonenberg N, Lopez Lastra M;
 XX
 DR WPI; 2005-122423/13.
 XX
 XX

PT Generating an established cell line that produces hepatitis C virus (HCV)
 PT for identifying a compound with anti-HCV activity, comprises transforming
 PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
 PT virus.
 XX
 PS Disclosure; Fig 57; 161pp; English.
 XX

CC The invention relates to generating an established cell line that
 CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
 CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
 CC Also included are a method for producing HCV in vitro, an EBV-established
 CC B-cell line capable of replicating complete and infectious HCV, a cell-
 CC based in vitro replication system for HCV (comprising an EBV-transformed
 CC B-cell capable of replicating complete and infectious HCV and a second
 CC population having HCV tropism and in which robust HCV replication occurs,
 CC so that under appropriate culture conditions the second population can
 CC become infected by the infectious HCV produced by the EBV-transformed B-
 CC cell), an assay for screening a test agent and selecting an agent that
 CC possesses anti-HCV activity and a method for identifying a compound with
 CC anti-HCV activity from a library of compounds. The method is useful in
 CC generating an established cell line that produces hepatitis C virus (HCV)
 CC for identifying a compound with anti-HCV activity. HCV sequence was
 CC amplified by reverse transcription from EBV-immortalized cell line 9.2
 CC (derived from patient PBMC samples), passaged through several changes in
 CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
 CC amplified from the infectious strain H77C. The present sequence is a PCR
 CC amplicon from the HCV sequence amplified from EBV cell line 9.2d.
 XX
 SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;
 Best Local Similarity 95.2%; Pred. No. 4;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
 |||||
 DB 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 44
 ADW15172
 ID ADW15172 standard; DNA; 131 BP.
 XX
 AC ADW15172;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE HCV from immortalized cell line 9.2b RT-PCR product #1.
 XX
 DE HCV from immortalized cell line 9.2b RT-PCR product #1.
 XX
 KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;
 KW infection; drug screening; ss; virucide; gene therapy;
 KW reverse transcriptase PCR.
 XX
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT mutation replace(70,G)
 FT /*tag= a
 FT mutation replace(82,A)
 FT /*tag= b
 XX
 PN WO2005005625-A2.
 XX
 PD 20-JAN-2005.
 XX
 PF 14-JUL-2004; 2004WO-CA001009.
 XX
 PR 14-JUL-2003; 2003CA-02436104.
 PR 06-FEB-2004; 2004CA-02454540.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Sonenberg N, Lopez Lastra M;
 XX
 DR WPI; 2005-122423/13.
 XX
 XX

PT Generating an established cell line that produces hepatitis C virus (HCV)
 PT for identifying a compound with anti-HCV activity, comprises transforming
 PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
 PT virus.
 XX
 PS Disclosure; Fig 57; 161pp; English.
 XX

CC The invention relates to generating an established cell line that
 CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
 CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
 CC Also included are a method for producing HCV in vitro, an EBV-established
 CC B-cell line capable of replicating complete and infectious HCV, a cell-
 CC based in vitro replication system for HCV (comprising an EBV-transformed
 CC B-cell capable of replicating complete and infectious HCV and a second
 CC population having HCV tropism and in which robust HCV replication occurs,
 CC so that under appropriate culture conditions the second population can
 CC become infected by the infectious HCV produced by the EBV-transformed B-
 CC cell), an assay for screening a test agent and selecting an agent that
 CC possesses anti-HCV activity and a method for identifying a compound with
 CC anti-HCV activity from a library of compounds. The method is useful in
 CC generating an established cell line that produces hepatitis C virus (HCV)
 CC for identifying a compound with anti-HCV activity. HCV sequence was
 CC amplified by reverse transcription from EBV-immortalized cell line 9.2
 CC (derived from patient PBMC samples), passaged through several changes in
 CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
 CC amplified from the infectious strain H77C. The present sequence is a PCR
 CC amplicon from the HCV sequence amplified from EBV cell line 9.2d.
 XX
 SQ Sequence 131 BP; 27 A; 42 C; 36 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;
 Best Local Similarity 95.2%; Pred. No. 4;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGTGAGGAAGTCTGCT 21
|||||
Db 6 CCTGTGAGGAAGTCTGCT 26

RESULT 45
ADM15173
ID ADM15173 standard; DNA; 131 BP.
XX
AC ADM15173;
XX
DT 07-APR-2005 (first entry)
XX
DE HCV from immortalized cell line 9.2c RT-PCR product #1.
XX
KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;
KW infection; drug screening; ss; virucide; gene therapy;
KW reverse transcriptase PCR.
XX
OS Hepatitis C virus.
XX
PN WO2005005625-A2.
XX
PD 20-JAN-2005.
XX
PF 14-JUL-2004; 2004WO-CA001009.
XX
PR 14-JUL-2003; 2003CA-02436104.
PR 06-FEB-2004; 2004CA-02454540.
XX
PA (UYMC-) UNIV MCGILL.
XX
XX Sonenberg N, Lopez Lastra M;
PI WPI; 2005-122423/13.
DR

XX Generating an established cell line that produces hepatitis C virus (HCV)
PT for identifying a compound with anti-HCV activity, comprises transforming
PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
PT virus.
XX

PS Disclosure; Fig 57; 161pp; English.

XX The invention relates to generating an established cell line that
CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
CC mononuclear cells (PBCs) that produce HCV with Epstein Barr virus (EBV).
CC Also included are a method for producing HCV in vitro, an EBV-established
CC B-cell line capable of replicating complete and infectious HCV, a cell-
CC based in vitro replication system for HCV (comprising an EBV-transformed
CC B-cell capable of replicating complete and infectious HCV and a second
CC population having HCV tropism and in which robust HCV replication occurs,
CC so that under appropriate culture conditions the second population can
CC become infected by the infectious HCV produced by the EBV-transformed B-
CC cell), an assay for screening a test agent and selecting an agent that
CC possesses anti-HCV activity and a method for identifying a compound with
CC anti-HCV activity from a library of compounds. The method is useful in
CC generating an established cell line that produces hepatitis C virus (HCV)
CC for identifying a compound with anti-HCV activity. HCV sequence was
CC amplified by reverse transcription from EBV-immortalized cell line 9.2
CC (derived from patient PBMC samples), passaged through several changes in
CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
CC amplified from the infectious strain H77C. The present sequence is a PCR
CC amplicon from the HCV sequence amplified from EBV cell line 9.2c.
XX

SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;
Best Local Similarity 95.2%; Pred. No. 4;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGTGAGGAAGTCTGCT 21
|||||

Db 6 CCTGTGAGGAAGTCTGCT 26

RESULT 46
AAZ57175
ID AAZ57175 standard; RNA; 133 BP.
XX
AC AAZ57175;
XX

DT 27-MAR-2000 (first entry)
XX
DE Human hepatitis C virus containing 133 mer RNA sequence.
XX
KW Bacteriophage SP6 promoter; single stranded RNA assay; diagnosis;
KW infectious disease; gene cloning; viral RNA; bacterial mRNA; ss.
XX

OS Hepatitis C virus.
OS Synthetic.
XX
PN EP969101-A1.
XX
PD 05-JAN-2000.
XX

PF 01-JUL-1999; 99EP-00112731.
XX
PR 01-JUL-1998; 98JP-00186434.
XX

PA (TOYJ) TOSOH CORP.

XX Ishiguro T, Saitoh J, Ishizuka T;
PI WPI; 2000-089306/08.
XX

PT Assaying single stranded RNA, to diagnose infectious diseases and to
PT determine the effects of therapeutic agents on the infectious diseases.
XX
PS Example 6; Page 13; 39pp; English.

XX A method has been developed for the assay of a single stranded RNA
CC containing a specific nucleic acid sequence in a sample at almost
CC constant temperature. The method is used to detect and quantify viral RNA
CC and bacterial mRNA and is used for diagnosis of infectious diseases and
CC in judging the effects of therapeutic agents for the infectious diseases.
CC large amounts of DNA and RNA can be produced containing a specific
CC nucleic acid sequence which is useful for cloning genes and exploring of the
CC unknown genes. The present sequence is used in the exemplification of the
CC present invention

SQ Sequence 133 BP; 30 A; 40 C; 36 G; 0 T; 27 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 3; Length 133;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGTGAGGAAGTCTGCT 21
|||||
Db 93 CCUGUGAGGAACUACUGUCU 113

RESULT 47
AAZ57775/C
ID AAZ57775 standard; DNA; 155 BP.
XX
AC AAZ57775;
XX

DT 05-APR-2000 (first entry)
XX
DE Hepatitis C virus antisense inhibitor oligonucleotide #41.

XX Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
OS Hepatitis C virus.

XX US6001990-A.
XX 14-DEC-1999.
XX 07-JUN-1995; 95US-00474700.
XX 10-MAY-1994; 94US-00240382.
XX (GEO) GEN HOSPITAL CORP.
XX Moradpour D, Wands JR, Wakita T;
XX WPI; 2000-104900/09.
XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections.
XX Claim 30; Col 33; 31pp; English.
XX This sequence is an antisense oligonucleotide that hybridizes to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
XX Sequence 155 BP; 29 A; 43 C; 51 G; 32 T; 0 U; 0 Other;
SQ Query Match 98.1%; Score 20.6; DB 3; Length 155;
Best Local Similarity 95.2%; Pred. No. 4.1;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGTGAGGAAGTCTGTCT 21
DB 113 CCTGTGAGGAAGTCTGTCT 93
RESULT 48
AD05716
ID ADR05716 standard; RNA; 210 BP.
XX ADR05716;
XX 04-NOV-2004 (first entry)
XX Hepatitis C virus UTR domain II-IIIb RNA fragment SEQ ID NO:29.
DE screening; identification; RNA regulatory element; reporter mRNA;
KW medicine; gene expression modulation; Hepatitis C virus; HCV;
KW untranslated region; UTR; gene; ss.
OS Hepatitis C virus.
XX WO2004067728-A2.
XX 12-AUG-2004.
XX 09-JAN-2004; 2004WO-US000423.
XX 17-JAN-2003; 2003US-0441028P.
XX (PTCT-) PTC THERAPEUTICS.
XX Pellegrini MC, Trotta CR, Huq SI;
XX WPI; 2004-581000/56.
XX Screening for and/or identifying (non-cell based) an RNA regulatory

PT element comprises combining a translation extract, an RNA test sequence,
PT and a reporter mRNA under conditions suitable for translation of the
XX reporter mRNA.
XX Example 2; SEQ ID NO 29; 87pp; English.
XX The present invention describes a non-cell based method of screening for
CC and/or identifying an RNA regulatory element. The method comprises
CC combining a translation extract, an RNA test sequence, and a reporter
CC mRNA under conditions suitable for translation of the reporter mRNA, and
CC measuring the effect of the test sequence on the translation of the
CC reporter mRNA, where a test sequence that modifies the translation of the
CC reporter mRNA includes an RNA regulatory element. Also described: (1) a
CC non-cell based method of screening for and/or identifying at least one
CC test compound which modulates the ability of an RJSTA sequence to
CC regulate translation of a reporter mRNA; (2) an in vitro translation
CC system for screening for and/or identifying a test compound, which
CC modulates the ability of an RNA regulatory sequence to regulate
CC translation of a reporter mRNA; (3) screening for and/or identifying a
CC test compound, which modulates the ability of an RNA regulatory sequence
CC to regulate translation of a reporter mRNA; (4) an in vitro translation
CC system for screening for and/or identifying a test compound capable of
CC reversing the inhibition of translation mediated by an RNA regulatory
CC sequence; (4) screening for and/or identifying a test compound, which
CC reverses inhibition of translation; and (5) a test compound identified
CC according to the method described above. The methods and systems are
CC useful for screening for and/or identifying an RNA regulatory element.
CC The test compound is useful for the manufacture of a medicine for
CC modulating the expression of a gene comprising the RNA sequence or of the
CC protein expressed from a construct engineered to include the RNA
CC sequence. The expression of the gene is aberrant in a disease state that
CC causes the survival and/or progression of a pathogenic organism. The
CC present sequence represents a Hepatitis C virus untranslated region (UTR)
CC RNA fragment, which is used in the exemplification of the present
CC invention.
XX Sequence 210 BP; 45 A; 64 C; 55 G; 0 T; 46 U; 0 Other;
SQ Query Match 98.1%; Score 20.6; DB 13; Length 210;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGTGAGGAAGTCTGTCT 21
DB 26 CCCUGUGAGGAACUACUGUCU 46
RESULT 49
AD05719
ID ADR05719 standard; RNA; 235 BP.
XX ADR05719;
XX 04-NOV-2004 (first entry)
XX Hepatitis C virus UTR domain II-IIIabc RNA fragment SEQ ID NO:32.
DE screening; identification; RNA regulatory element; reporter mRNA;
KW medicine; gene expression modulation; Hepatitis C virus; HCV;
KW untranslated region; UTR; gene; ss.
OS Hepatitis C virus.
XX WO2004067728-A2.
XX 12-AUG-2004.
XX 09-JAN-2004; 2004WO-US000423.
XX 17-JAN-2003; 2003US-0441028P.
XX (PTCT-) PTC THERAPEUTICS.
XX

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 03:55:23 ; Search time 894 Seconds
(without alignments)
1335.249 Million cell updates/sec

Title: US-10-070-415A-1
Perfect score: 21
Sequence: 1 cccgtgagggaactwtgtct 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vl.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	98.1	21	6	BD178495
2	20.6	98.1	21	6	BD182888
3	20.6	98.1	24	6	AX003352
4	20.6	98.1	24	6	AX470074
5	20.6	98.1	24	6	AX470078
6	20.6	98.1	24	6	AX470079
7	20.6	98.1	25	6	AR593796
8	20.6	98.1	27	6	A39029
9	20.6	98.1	27	6	AR063363
10	20.6	98.1	27	6	AR123554
11	20.6	98.1	27	6	AR267295
12	20.6	98.1	27	6	AR305705
13	20.6	98.1	27	6	AR654197
14	20.6	98.1	27	6	AR655174
15	20.6	98.1	27	6	AX023091
16	20.6	98.1	27	6	AX398128
17	20.6	98.1	27	6	AX417297
18	20.6	98.1	28	6	AR094964

19	20.6	98.1	28	6	AR094991
20	20.6	98.1	31	6	E11709
c 21	20.6	98.1	45	6	BD069486
22	20.6	98.1	45	6	BD083958
c 23	20.6	98.1	45	6	AR338407
c 24	20.6	98.1	45	6	AR353602
c 25	20.6	98.1	45	6	AR636812
c 26	20.6	98.1	51	6	I73300
c 27	20.6	98.1	67	6	AR095004
28	20.6	98.1	73	6	BD171247
29	20.6	98.1	80	6	CQ830528
30	20.6	98.1	131	13	CS001589
31	20.6	98.1	131	13	CS001590
32	20.6	98.1	131	13	CS001591
33	20.6	98.1	131	13	CS001592
34	20.6	98.1	131	13	CS001593
35	20.6	98.1	131	13	CS001594
c 36	20.6	98.1	155	6	AR095003
37	20.6	98.1	232	13	AF506627
38	20.6	98.1	232	13	AF506629
39	20.6	98.1	232	13	AF506666
40	20.6	98.1	232	13	AF506679
41	20.6	98.1	238	6	BD182732
42	20.6	98.1	238	6	BD182733
43	20.6	98.1	238	6	BD182735
44	20.6	98.1	238	13	AF506647
45	20.6	98.1	238	13	AF506655
46	20.6	98.1	239	6	BD182734
47	20.6	98.1	239	13	AF506683
48	20.6	98.1	242	13	AF506687
49	20.6	98.1	258	13	AY344040
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51	20.6	98.1	260	6	AR655260
52	20.6	98.1	260	6	AR655261
53	20.6	98.1	260	6	AR655262
54	20.6	98.1	265	13	CS001586
55	20.6	98.1	265	13	CS001587
56	20.6	98.1	266	13	CS001585
57	20.6	98.1	267	6	AX398192
58	20.6	98.1	278	6	AX398190
59	20.6	98.1	280	13	AY344026
60	20.6	98.1	291	13	HPCSNOCR
61	20.6	98.1	296	13	HPCBR56A
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63	20.6	98.1	299	6	AX171760
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87	20.6	98.1	327	13	AY8344219
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 94 20.6 98.1 340 13 HPC5NR4 D31604 Human hepat
 95 20.6 98.1 340 13 HPC5NR5 D31605 Human hepat
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 99 20.6 98.1 341 6 AR119857 Sequence
 100 20.6 98.1 341 6 AR153763 Sequence

ALIGNMENTS

RESULT 1
 BD178495
 LOCUS BD178495 21 bp DNA linear PAT 16-APR-2003
 DEFINITION Method of detecting nucleic acid relating to disease.
 ACCESSION BD178495
 VERSION BD178495.1 GI:30015761
 KEYWORDS WO 02077281-A/1.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
 TITLE Method of detecting nucleic acid relating to disease
 JOURNAL Patent: WO 02077281-A 1 03-OCT-2002;
 TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
 YASUHIKO OTA

COMMENT OS Hepatitis virus (hepatitis C virus)
 PN WO 02077281-A/1
 PD 03-OCT-2002
 PF 05-MAR-2002 WO 2002JP002030
 PR 27-MAR-2001 JP 01P 090053.18-SEP-2001 JP 01P 284112 PI
 KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
 C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
 G01N33/576,
 PC G01N37/00
 CC Method of detecting nucleic acid relating to disease FH Key
 FT source 1..21
 FT /organism='Hepatitis virus (hepatitis C virus)'

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ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 21;
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QY 1 CCCTGTGAGGAAGTCTGTCT 21
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DB 1 CCCTGTGAGGAAGTCTGTCT 21
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 BD182888
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 DEFINITION Detection of nucleic acid associated with disease.
 ACCESSION BD182888
 VERSION BD182888.1 GI:31875088
 KEYWORDS JP 2002355083-A/1.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
 TITLE Detection of nucleic acid associated with disease

JOURNAL

Patent: JP 2002355083-A 1 10-DEC-2002;
 TOSHIBA CORP
 OS Hepatitis virus (hepatitis C virus)
 PN JP 2002355083-A/1
 PD 10-DEC-2002
 PF 26-MAR-2002 JP 2002086681
 PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
 C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
 G01N33/569,
 PC G01N33/576// (C12Q1/68, C12R1/93), C12N15/00, C12N15/00 CC
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DB 1 CCCTGTGAGGAAGTCTGTCT 21
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RESULT 3
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 LOCUS AX003352 24 bp DNA linear PAT 24-AUG-2000
 DEFINITION Sequence 3 from Patent WO9928503.
 ACCESSION AX003352
 VERSION AX003352.1 GI:9927157
 KEYWORDS
 SOURCE Hepatitis C virus
 ORGANISM Hepatitis C virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Hepacivirus.

REFERENCE 1
 AUTHORS Primi,D. and Mantero,G.
 TITLE Methods of detecting polynucleotide analytes
 JOURNAL Patent: WO 9928503-A 3 10-JUN-1999;
 PRIMI DANIELE (IT); MANTERO GIOVANNI (IT)

FEATURES

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RESULT 4

AX470074
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 DEFINITION Sequence 1 from Patent WO02052041.
 ACCESSION AX470074
 VERSION AX470074.1 GI:22205310
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE 1
AUTHORS Gessner, M.
TITLE 5' nuclease nucleic acid amplification assay having an improved internal control
JOURNAL Patent: WO 02052041-A 1 04-JUL-2002;
Baxter Aktiengesellschaft (AT)
FEATURES Location/Qualifiers
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Qy 1 CCCTGTGAGGAACCTGCTCT 21
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Db 1 CCCTGTGAGGAACCTGCTCT 21

RESULT 5
AX470078 24 bp DNA linear PAT 09-AUG-2002
LOCUS Sequence 5 from Patent WO02052041.
DEFINITION AX470078
ACCESSION AX470078
VERSION AX470078.1 GI:22205314
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Gessner, M.
TITLE 5' nuclease nucleic acid amplification assay having an improved internal control
JOURNAL Patent: WO 02052041-A 5 04-JUL-2002;
Baxter Aktiengesellschaft (AT)
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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
AX470079 24 bp DNA linear PAT 09-AUG-2002
LOCUS Sequence 6 from Patent WO02052041.
DEFINITION AX470079
ACCESSION AX470079
VERSION AX470079.1 GI:22205315
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Gessner, M.
TITLE 5' nuclease nucleic acid amplification assay having an improved internal control
JOURNAL Patent: WO 02052041-A 6 04-JUL-2002;
Baxter Aktiengesellschaft (AT)
FEATURES Location/Qualifiers

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Best Local Similarity 95.2%; Pred. No. 5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCCTGTGAGGAACCTGCTCT 21

RESULT 7
AR593796 25 bp DNA linear PAT 15-DEC-2004
LOCUS Sequence 1 from patent US 6811974.
DEFINITION AR593796
ACCESSION AR593796
VERSION AR593796.1 GI:56643301
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hu, Y.-W.
TITLE Primer-specific and mismatch extension assay for identifying gene variation
JOURNAL Patent: US 6811974-A 1 02-NOV-2004;
Canadian Blood Services; Ottawa;
CAX;
FEATURES Location/Qualifiers
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Db 4 CCCTGTGAGGAACCTGCTCT 24

RESULT 8
A39029 27 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 1 from Patent WO9412670.
DEFINITION A39029
ACCESSION A39029
VERSION A39029.1 GI:2295415
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Maertens, G., Stuyver, L., Roseau, R. and Van, H.H.
TITLE PROCESS FOR TYPING OF HCV ISOLATES
JOURNAL Patent: WO 9412670-A 1 09-JUN-1994;
INNOGENETICS NV (BE)
COMMENT Other publication AU 5628294 940622
Other publication CA 2128528 940609
Other publication JP 7503143T 950406.
FEATURES Location/Qualifiers
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REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 5846704-A 1 08-DEC-1998;					
JOURNAL					
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1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 6171784-A 1 09-JAN-2001;					
JOURNAL					
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REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 6887985-A 1 03-MAY-2005;					
JOURNAL					
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1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing HCV isolates					
TITLE					
Patent: US 6548244-A 1 15-APR-2003;					
JOURNAL					
Innogenetics N.V.; Ghent;					
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1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 6887985-A 1 03-MAY-2005;					
JOURNAL					
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1 (bases 1 to 27)					
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AUTHORS					
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Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
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REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
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1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
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AUTHORS					
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REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
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ORGANISM					
Unknown.					
REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 6887985-A 1 03-MAY-2005;					
JOURNAL					
Location/Qualifiers					
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DB 6;					
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Mismatches					
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Indels					
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Gaps					
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Qy					
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CCCTGTGAGGAAGTCTGTCT 21					
Db					
1					
CCCTGTGAGGAAGTCTGTCT 21					
RESULT 20					
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LOCUS					
DEFINITION					
Sequence 1 from patent US 6887985.					
ACCESSION					
AR654197					
VERSION					
AR654197.1					
GI:67585157					
KEYWORDS					
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ORGANISM					
Unknown.					
REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 6887985-A 1 03-MAY-2005;					
JOURNAL					
Location/Qualifiers					
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DB 6;					
Length 27;					
Matches					
21;					
Conservative					
0;					
Mismatches					
0;					
Indels					
0;					
Gaps					
0;					
Qy					
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CCCTGTGAGGAAGTCTGTCT 21					
Db					
1					
CCCTGTGAGGAAGTCTGTCT 21					
RESULT 21					
AR654197					
LOCUS					
DEFINITION					
Sequence 1 from patent US 6887985.					
ACCESSION					
AR654197					
VERSION					
AR654197.1					
GI:67585157					
KEYWORDS					
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ORGANISM					
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REFERENCE					
1 (bases 1 to 27)					
Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
AUTHORS					
Process for typing of HCV isolates					
TITLE					
Patent: US 6887985-A 1 03-MAY-2005;					
JOURNAL					
Location/Qualifiers					
FEATURES					
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DB 6;					
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Matches					
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Conservative					
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Mismatches					
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Indels					
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Gaps					
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Qy					
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CCCTGTGAGGAAGTCTGTCT 21					
Db					
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RESULT 22					
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LOCUS					
DEFINITION					
Sequence 1 from patent US 6887985.					
ACCESSION					
AR654197					
VERSION					
AR654197.1					
GI:67585157					
KEYWORDS					
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ORGANISM					
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REFERENCE					
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ORIGIN
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 14
LOCUS AR655174 27 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 1 from patent US 6891026.
ACCESSION AR655174
VERSION AR655174.1 GI:67586961
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing of HCV isolates
JOURNAL Patent: US 6891026-A 1 10-MAY-2005;
Innogenetics N.V.; Ghent;
EPX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 15
LOCUS AX023091 27 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 1 from Patent EP0905258.
ACCESSION AX023091
VERSION AX023091.1 GI:10046556
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Maertens,G., Stuyver,L., Rossau,R., Stuyver,L. and van Heuverswyn,H.
TITLE Detection and typing of hcv using 5'utr and ns5 nucleic acid
JOURNAL Patent: EP 0905258-A 1 31-MAR-1999;
Innogenetics NV (BE)
FEATURES
source Location/Qualifiers
1..27
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/isolate="HCV (KATO ET AL., 1992)"
/db_xref="taxon:11103"
/map="POSITION -299 OF 5' END"
misc_feature 1..27
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 16
LOCUS AX398128 27 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 5 from Patent WO0220837.
ACCESSION AX398128
VERSION AX398128.1 GI:21260943
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ronaghi,M., Ekstroem,B. and Pourmand,N.
TITLE Method
JOURNAL Patent: WO 0220837-A 5 14-MAR-2002;
Pyrosequencing AB (SE) ; The Board of Trustees of The Leland
Stanford Junior University (US)
LOCATION/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide HCV-PCR-OUTF"

ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 17
LOCUS AX417297 27 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent EP1197568.
ACCESSION AX417297
VERSION AX417297.1 GI:21522601
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Maertens,G., Rossau,R., Stuyver,L. and van Heuverswyn,H.
TITLE Detection and typing of hcv using 5'utr and ns5 nucleic acid
JOURNAL Patent: EP 1197568-A 1 17-APR-2002;
Innogenetics N.V. (BE)
FEATURES
source Location/Qualifiers
1..27
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 18
LOCUS AX417297 27 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent EP1197568.
ACCESSION AX417297
VERSION AX417297.1 GI:21522601
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Maertens,G., Rossau,R., Stuyver,L. and van Heuverswyn,H.
TITLE Detection and typing of hcv using 5'utr and ns5 nucleic acid
JOURNAL Patent: EP 1197568-A 1 17-APR-2002;
Innogenetics N.V. (BE)
FEATURES
source Location/Qualifiers
1..27
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/mol_type="unassigned DNA"
/db_xref="taxon:11103"

ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 1 CCTGTGAGGAAGTCTGTCT 21
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RESULT 18
AR094964/c
LOCUS       AR094964                28 bp    DNA
DEFINITION   Sequence 2 from patent US 6001990.
ACCESSION   AR094964
VERSION     AR094964.1  GI:10022381
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 28)
AUTHORS   Wands,J.R., Wakita,T. and Moradpour,D.
TITLE     Antisense inhibition of hepatitis C virus
JOURNAL   Patent: US 6001990-A 2 14-DEC-1999;
FEATURES   source
            1..28
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      98.1%; Score 20.6; DB 6; Length 28;
Best Local Similarity 95.2%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21
    |||||:|||||:|||||
Db 23 CCTGTGAGGAACTACTGTCT 3

RESULT 19
AR094991
LOCUS       AR094991                28 bp    DNA
DEFINITION   Sequence 29 from patent US 6001990.
ACCESSION   AR094991
VERSION     AR094991.1  GI:10022435
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 28)
AUTHORS   Wands,J.R., Wakita,T. and Moradpour,D.
TITLE     Antisense inhibition of hepatitis C virus
JOURNAL   Patent: US 6001990-A 29 14-DEC-1999;
FEATURES   Location/Qualifiers
            source
            1..28
            /organism="unknown"
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ORIGIN
Query Match      98.1%; Score 20.6; DB 6; Length 28;
Best Local Similarity 95.2%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21
    |||||:|||||:|||||
Db 23 CCTGTGAGGAACTACTGTCT 3

RESULT 20
E11709
LOCUS       E11709                 31 bp    DNA
DEFINITION   PCR primer for detecting minus chain of hepatitis C virus.
ACCESSION   E11709
VERSION     E11709.1  GI:22025345
KEYWORDS    JP 1996187097-A/3.
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 31)
AUTHORS   Yamaguchi,K., Matsunaga,Y. and Fukutani,T.
TITLE     SPECIFIC DETECTING METHOD OF PLUS STRAND OR MINUS STRAND GENE OF

RNA VIRUS
Patent: JP 1996187097-A 3 23-JUL-1996;
TONEN CORP
OS      None
OC      Artificial sequences.
PN      JP 1996187097-A/3
PD      23-JUL-1996
PF      28-DEC-1994  JP 1994338535
PI      YAMAGUCHI KENJIRO, MATSUNAGA YUKA, FUKUTANI TOYOJI PC
C12Q1/68,C12N15/09,C12Q1/70;
CC      strandedness: Single;
CC      topology: Linear;
CC      hypothetical: No;
CC      anti-sense: No; Location/Qualifiers
FH      Key
FT      source      1..31
FT      misc_feature 1..31 /notes='PCR primer,T-31'.
FT      Location/Qualifiers
            1..31
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      98.1%; Score 20.6; DB 6; Length 31;
Best Local Similarity 95.2%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21
    |||||:|||||:|||||
Db 11 CCTGTGAGGAACTACTGTCT 31

RESULT 21
BD069486/c
LOCUS       BD069486                45 bp    DNA
DEFINITION   Nucleic acid amplification method: Ramification-extension
            amplification method (RAM).
ACCESSION   BD069486
VERSION     BD069486.1  GI:22615089
KEYWORDS    JP 2001514483-A/22.
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 45)
AUTHORS   Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.
TITLE     Nucleic acid amplification method: Ramification-extension
            amplification method (RAM)
JOURNAL   Patent: JP 2001514483-A 22 11-SEP-2001;
            DAVID Y ZHANG,MARGARET BRANDWEIN,TERENCE C H HSUIH
COMMENT    OS      Unidentified
            PN      JP 2001514483-A/22
            PD      11-SEP-2001
            PF      30-JUL-1997  JP 1998509122
            PI      31-JUL-1996  US 08/690494
            PR      DAVID Y ZHANG,MARGARET BRANDWEIN,TERENCE C H HSUIH PC
            C12Q1/68,C12Q1/70,C12P19/34,C07H21/02,C07H21/04 CC      Strandedness:
            Single;
            CC      Topology: Linear;
            CC      Nucleic acid amplification method: Ramification-extension
            amplification
            CC      method (RAM)
            FH      Key
            FT      source      1..45
            FT      Location/Qualifiers
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            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
FEATURES   source
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ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||:|||||:|||||
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 22
BD083958/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD083958 45 bp DNA linear PAT 27-AUG-2002
Nucleic acid amplification method: Hybridization signal
amplification method (HSAM).
BD083958
BD083958.1 GI:22629568
JP 2001521373-A/22.
unidentified
unclassified.
1 (bases 1 to 45)
Zhang,D.Y. and Brandwein,M.
Nucleic acid amplification method: Hybridization signal
amplification method (HSAM)
Patent: JP 2001521373-A 22 06-NOV-2001;
DAVID Y ZHANG,MARGARET BRANDWEIN
OS Unidentified
PN JP 2001521373-A/22
PD 06-NOV-2001
PF 30-JUL-1997 JP 1998509121
PR 31-JUL-1996 US 08/690495
PI DAVID Y ZHANG,MARGARET BRANDWEIN
PC C12Q1/68,C12Q1/70,C12P19/34,C07H21/04 CC
Strandedness: Single;
CC Topology: Linear;
CC Nucleic acid amplification method: Hybridization signal CC
amplification
CC method (HSAM) Location/Qualifiers
FH Key 1..45
FT source /organism='Unidentified'.
Location/Qualifiers
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ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 23
AR338407/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AR338407 45 bp DNA linear PAT 17-AUG-2003
Sequence 22 from patent US 6569647.
AR338407
AR338407.1 GI:33725179
Unidentified.
Unknown.
1 (bases 1 to 45)
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.
Nucleic acid amplification method: ramification-extension
amplification method (RAM)

JOURNAL

Mount Sinai School of Medicine of New York University; New York, NY

Patent: US 6569647-A 22 27-MAY-2003;
Mount Sinai School of Medicine of New York University; New York, NY

Location/Qualifiers
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/mol_type='genomic DNA'

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 24
AR353602/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR353602 45 bp DNA linear PAT 17-AUG-2003
Sequence 22 from patent US 6593086.
AR353602
AR353602.1 GI:33759633
Unknown.
Unknown.
1 (bases 1 to 45)
Zhang,D.Y.
Nucleic acid amplification methods
Patent: US 6593086-A 22 15-JUL-2003;
Mount Sinai School of Medicine of New York University; New York, NY

Location/Qualifiers
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/organism='unknown'
/mol_type='genomic DNA'

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||:|||||:|||||
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 25
AR636812/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR636812 45 bp DNA linear PAT 20-APR-2005
Sequence 22 from patent US 6855523.
AR636812
AR636812.1 GI:62769941
Unknown.
Unknown.
1 (bases 1 to 45)
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.
Nucleic acid amplification method: ramification-extension
amplification method (RAM)
Patent: US 6855523-A 22 15-FEB-2005;
Mount Sinai School of Medicine of New York University; New York, NY

Location/Qualifiers
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/organism='unknown'
/mol_type='genomic DNA'

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||:|||||:|||||
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 26
AR636812/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR636812 45 bp DNA linear PAT 20-APR-2005
Sequence 22 from patent US 6855523.
AR636812
AR636812.1 GI:62769941
Unknown.
Unknown.
1 (bases 1 to 45)
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.
Nucleic acid amplification method: ramification-extension
amplification method (RAM)
Patent: US 6855523-A 22 15-FEB-2005;
Mount Sinai School of Medicine of New York University; New York, NY

Location/Qualifiers
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/organism='unknown'
/mol_type='genomic DNA'

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
|||||:|||||:|||||
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 27
AR636812/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR636812 45 bp DNA linear PAT 20-APR-2005
Sequence 22 from patent US 6855523.
AR636812
AR636812.1 GI:62769941
Unknown.
Unknown.
1 (bases 1 to 45)
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.
Nucleic acid amplification method: ramification-extension
amplification method (RAM)

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QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 31 CCCTGTGAGGAACACTACTGTCT 11

RESULT 26
LOCUS I73300 51 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 31 from patent US 5686272.
ACCESSION I73300
VERSION I73300.1 GI:3009439
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 31 11-NOV-1997;
FEATURES
    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"
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Query Match 98.1%; Score 20.6; DB 6; Length 51;
Best Local Similarity 95.2%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 16 CCCTGTGAGGAACACTACTGTCT 36

RESULT 27
LOCUS AR095004/c 67 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 42 from patent US 6001990.
ACCESSION AR095004
VERSION AR095004.1 GI:10022461
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 67)
AUTHORS Wands,J.R., Wakita,T. and Moradpour,D.
TITLE Antisense inhibition of hepatitis C virus
JOURNAL Patent: US 6001990-A 42 14-DEC-1999;
FEATURES
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            /organism="unknown"
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ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 67;
Best Local Similarity 95.2%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 25 CCCTGTGAGGAACACTACTGTCT 5

RESULT 28
LOCUS BD171247 73 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of detecting pathogenic microorganism.
ACCESSION BD171247
VERSION BD171247.1 GI:27877059
KEYWORDS WO 02052043-A/39,
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE 1 (bases 1 to 73)
AUTHORS Shimada,M., Hino,F. and Kato,I.
TITLE Method of detecting pathogenic microorganism
JOURNAL Patent: WO 02052043-A 39 04-JUL-2002;
COMMENT TAKARA SHUZO CO LTD,MASAMITSU SHIMADA,FUMITSUGU HINO,IKUNOSHIN KATO
OS Artificial Sequence
PN WO 02052043-A/39
PD 04-JUL-2002
PF 26-DEC-2001 WO 2001JP011422
PR 28-DEC-2000 JP OOP 396222,26-DEC-2000 JP OOP 396321 PR
29-JUN-2001 JP O1P 199552,13-SEP-2001 JP O1P 278920 PI
MASAMITSU SHIMADA,FUMITSUGU HINO,IKUNOSHIN KATO PC
C12Q1/68,C12N15/09
CC Primer area to amplify a portion of HCV.
FH Key
FT source
    Location/Qualifiers
        1..73
            /organism='Artificial Sequence'.
FEATURES
    source
        Location/Qualifiers
            1..73
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 73;
Best Local Similarity 95.2%; Pred. No. 4.6;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 21 CCCTGTGAGGAACACTACTGTCT 41

RESULT 29
LOCUS CQ830528 80 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 2 from Patent WO2004055210.
ACCESSION CQ830528
VERSION CQ830528.1 GI:50250861
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Balakireva,I.
TITLE Molecules inhibiting hepatitis c virus protein synthesis and method
for screening same
JOURNAL Patent: WO 2004055210-A 2 01-JUL-2004;
UNIVERSITE JOSEPH FOURIER (FR)
FEATURES
    Location/Qualifiers
        1..80
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="R gion II de l'RES de VHC"
ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 80;
Best Local Similarity 95.2%; Pred. No. 4.6;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 4 CCCTGTGAGGAACACTACTGTCT 24

RESULT 30
LOCUS CS001589 131 bp DNA linear VRL 01-FEB-2005
DEFINITION Sequence 5 from Patent WO20050505625.
ACCESSION CS001589
VERSION CS001589.1 GI:58424011
KEYWORDS

```

SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; sgRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Sonenberg, N. and Lopez Lastra, M.
TITLE Method for inducing hepatitis C virus (hcv) replication in vitro,
cells and cell lines enabling robust hcv replication and kit
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;
McGill University (CA)
FEATURES source
Location/Qualifiers
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/mol_type="unassigned DNA"
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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 31
CS001590
LOCUS 131 bp DNA linear VRL 01-FEB-2005
DEFINITION Sequence 6 from Patent WO2005005625.
ACCESSION CS001590
VERSION CS001590.1 GI:58424012
KEYWORDS
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)
ORGANISM Cercopithecine herpesvirus 15
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1
AUTHORS Sonenberg, N. and Lopez Lastra, M.
TITLE Method for inducing hepatitis C virus (hcv) replication in vitro,
cells and cell lines enabling robust hcv replication and kit
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;
McGill University (CA)
FEATURES source
Location/Qualifiers
1..131
/organism="Cercopithecine herpesvirus 15"
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/db_xref="taxon:45455"

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Best Local Similarity 95.2%; Pred. No. 4.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 32
CS001591
LOCUS 131 bp DNA linear VRL 01-FEB-2005
DEFINITION Sequence 7 from Patent WO2005005625.
ACCESSION CS001591
VERSION CS001591.1 GI:58424013
KEYWORDS
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)
ORGANISM Cercopithecine herpesvirus 15
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1

AUTHORS Sonenberg, N. and Lopez Lastra, M.
TITLE Method for inducing hepatitis C virus (hcv) replication in vitro,
cells and cell lines enabling robust hcv replication and kit
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;
McGill University (CA)
FEATURES source
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Best Local Similarity 95.2%; Pred. No. 4.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 33
CS001592
LOCUS 131 bp DNA linear VRL 01-FEB-2005
DEFINITION Sequence 8 from Patent WO2005005625.
ACCESSION CS001592
VERSION CS001592.1 GI:58424014
KEYWORDS
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)
ORGANISM Cercopithecine herpesvirus 15
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1
AUTHORS Sonenberg, N. and Lopez Lastra, M.
TITLE Method for inducing hepatitis C virus (hcv) replication in vitro,
cells and cell lines enabling robust hcv replication and kit
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;
McGill University (CA)
FEATURES source
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QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 34
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LOCUS 131 bp DNA linear VRL 01-FEB-2005
DEFINITION Sequence 9 from Patent WO2005005625.
ACCESSION CS001593
VERSION CS001593.1 GI:58424015
KEYWORDS
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)
ORGANISM Cercopithecine herpesvirus 15
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1
AUTHORS Sonenberg, N. and Lopez Lastra, M.
TITLE Method for inducing hepatitis C virus (hcv) replication in vitro,
cells and cell lines enabling robust hcv replication and kit
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;


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RESULT 39
AF506666      232 bp RNA linear VRL 20-MAY-2002
LOCUS Hepatitis C virus isolate KMA22 5' untranslated region, partial
DEFINITION
ACCESSION AF506666
VERSION AF506666
KEYWORDS AF506666.1 GI:20978010
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 232)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 232)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
LOCATION/Qualifiers
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5'UTR
ORIGIN

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Db 3 CCCTGTGAGGAAGTCTGTCT 23

RESULT 41
BD182732      238 bp DNA linear PAT 17-JUN-2003
LOCUS Profile database and method for preparing profile.
DEFINITION
ACCESSION BD182732
VERSION BD182732.1 GI:31874932
KEYWORDS JP 2002358309-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 238)
AUTHORS Yatsuka,S., Muto,I., Yamashita,I. and Tamura,T.
TITLE Profile database and method for preparing profile
JOURNAL Patent: JP 2002358309-A 2 13-DEC-2002;
HITACHI SOFTWARE ENGINEERING CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2002358309-A/2
PD 13-DEC-2002
PF 04-JUN-2001 JP 2001168230
PI SHIGERU YATSUKA, ISAMU MUTO, IWAO YAMASHITA, TAKURO TAMURA PC
G06F17/30//C12N15/09,C12Q1/68,C12N15/00
CC Profile database and method for preparing profile FH Key
LOCATION/Qualifiers
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ORIGIN

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Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 42
BD182733      238 bp DNA linear PAT 17-JUN-2003
LOCUS Profile database and method for preparing profile.
DEFINITION
ACCESSION BD182733
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Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 3 CCCTGTGAGGAAGTCTGTCT 23

RESULT 46

BD182734 239 bp DNA linear PAT 17-JUN-2003
LOCUS
DEFINITION Profile database and method for preparing profile.
ACCESSION BD182734
VERSION BD182734.1 GI:31874934
KEYWORDS JP 2002358309-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE 1 (bases 1 to 239)

Yatsuka,S., Muto,I., Yamashita,I. and Tamura,T.
Profile database and method for preparing profile
Patent: JP 2002358309-A 4 13-DEC-2002;

HITACHI SOFTWARE ENGINEERING CO LTD

OS Homo sapiens (human)

PN JP 2002358309-A/4

PD 13-DEC-2002

PF 04-JUN-2001 JP 2001168230

PI SHIGERU YATSUKA, ISAMU MUTO, IWAO YAMASHITA, TAKURO TAMURA PC
G06F17/30//C12N15/09, C12Q1/68, C12N15/00

CC Profile database and method for preparing profile PH Key
FT Location/Qualifiers

FT source 1..239
/organism="Homo sapiens (human)"

Location/Qualifiers

1..239

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ORIGIN

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Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 47

AF506683 239 bp RNA linear VRL 20-MAY-2002
LOCUS
DEFINITION Hepatitis C virus isolate KGV54 5' untranslated region, partial
sequence.

ACCESSION AF506683

VERSION AF506683.1 GI:20978027

KEYWORDS

SOURCE

ORGANISM

Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1 (bases 1 to 239)

AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
REFERENCE 2 (bases 1 to 239)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia

FEATURES
source

1..239 Location/Qualifiers
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/country="Russia"
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ORIGIN

Query Match 98.1%; Score 20.6; DB 13; Length 239;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21

|||||:|||||:|||||

Db 3 CCCTGTGAGGAAGTCTGTCT 23

RESULT 48

AF506687

LOCUS

DEFINITION Hepatitis C virus isolate KMA3 5' untranslated region, partial
sequence.

ACCESSION AF506687

VERSION AF506687.1 GI:20978031

KEYWORDS

SOURCE

ORGANISM

Hepatitis C virus

Hepatitis C virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Genetic variability of hepatitis C virus in Western Siberia

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Direct Submission

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Direct Submission

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Direct Submission

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Direct Submission

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Direct Submission

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

Direct Submission

TITLE

JOURNAL

REFERENCE 2 (bases 1 to 242)

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

ACCESSION AY344040
VERSION AY344040.1 GI:37790679
KEYWORDS
SOURCE
ORGANISM
Hepatitis C virus
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE
AUTHORS
1 (bases 1 to 258)
Bhattacharyya, S., Mapa, K., Prabhavathi, S., Sudhamani, S.R.,
Menon, P.K., John, K.P., Shivaram, C., Amarnath, S. and Das, S.
Phylogenetic conservation of the stem-loop III structure of the
5' untranslated region of Hepatitis C virus RNA among natural
variants in samples collected from Southern India
Arch. Virol. 149 (5), 1015-1026 (2004)

JOURNAL
PUBMED
15098115
REFERENCE
2 (bases 1 to 258)
Bhattacharyya, S., Prabhavathi, S., Mapa, K. and Das, S.
Direct Submission
TITLE
Submitted (16-JUL-2003) Microbiology & Cell Biology, Indian
Institute of Science, C.V. Raman Street, Bangalore, Karnataka
560012, India

FEATURES
Location/Qualifiers
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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 21 CCCTGTGAGGAAGTCTGTCT 41

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LOCUS
DEFINITION Sequence 40 from patent US 6001990.
ACCESSION AR095002
VERSION AR095002.1 GI:10022457
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS
1 (bases 1 to 260)
Wands, J.R., Wakita, T. and Moradpour, D.
TITLE Antisense inhibition of hepatitis C virus
JOURNAL Patent: US 6001990-A 40 14-DEC-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 218 CCCTGTGAGGAAGTCTGTCT 198

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 496997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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- 13: geneseqn2004bs.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	95.2	581	10	ABX08685 Pathogeni
4	20	95.2	581	10	ABX08683 Pathogeni
5	20	95.2	581	10	ABX08684 Pathogeni
6	20	95.2	581	12	ADL92264 Human MxA
7	19.4	92.4	46	12	ADL92256 Human MxA
8	19.4	92.4	132	12	ADO78057 Human MxA
9	19.4	92.4	132	12	ADO78056 Human MxA
10	19.4	92.4	581	4	AAI70373 Human MxA
11	19.4	92.4	581	4	AAI70375 Human MxA
12	19.4	92.4	581	4	AAI70376 Human MxA
13	19.4	92.4	581	4	AAI70374 Human MxA
14	19.4	92.4	581	5	AAI70353 Promoter
15	19.4	92.4	581	5	AAI70350 Promoter
16	19.4	92.4	581	5	AAI70352 Promoter
17	19.4	92.4	581	5	AAI70351 Promoter
18	19.4	92.4	581	10	ABX08706 Pathogeni
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23	19.4	92.4	2451	9	AAJ55593 Human MxA
24	19.4	92.4	5376	9	AAJ55595 Luciferas
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30	17.8	84.8	581	12	ADL92268 Human MxA
31	17.8	84.8	581	6	ABL34192 Human imm
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34	17	81.0	3302	13	ADR14356 Human NF-
35	17	81.0	3302	14	ADL07310 Cyclin-de
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37	17	81.0	3302	14	ABE56452 Radiochem
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44	16.8	80.0	2179	5	AAJ589697 DNA encod
45	16.8	80.0	2250	5	AAJ593754 DNA encod
46	16.8	80.0	2830	5	AAJ593758 DNA encod
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58	16.8	80.0	9072	2	AAV74356 Staphyloc
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61	16.4	78.1	2394	12	ADQ76241 Bacillus
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67	16.2	77.1	648	2	AAQ91406 Human olf
68	16.2	77.1	945	4	AAH32454 Human olf
69	16.2	77.1	945	4	AAH32461 Human olf
70	16.2	77.1	945	4	AAH31761 Human olf
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73	16.2	77.1	989	6	ABT04154 Human G-p
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80	16.2	77.1	1110	8	ACC50556 Human sec
81	16.2	77.1	1110	10	ADA56193 Gene enco
82	16.2	77.1	1146	5	AAJ71758 DNA encod
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88	16.2	77.1	1713	12	ADP04057 Human col
89	16.2	77.1	2000	10	ACC60728 Gene sequ
90	16.2	77.1	2000	10	ADK61825 Disease t
91	16.2	77.1	2746	13	ADT18862 Plant CDN
92	16.2	77.1	3009	13	ADS46635 Bacterial

C 93 16.2 77.1 5491 13 ACN43580 Human dia
C 94 16.2 77.1 5492 13 ACN43579 Human dia
C 95 16.2 77.1 5519 12 ADQ83246 Human tum
C 96 16.2 77.1 5519 12 ADQ86334 Human tum
C 97 16.2 77.1 5519 12 ADQ83923 Human tum
C 98 16.2 77.1 5519 12 ADQ84399 Human tum
C 99 16.2 77.1 5519 13 ADQ85153 Human tum
C 100 16.2 77.1 5519 14 ADZ49355 Insulin s

ALIGNMENTS

RESULT 1
ABX08703
ID ABX08703 standard; DNA; 581 BP.
AC ABX08703;
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DT 20-JAN-2003 (first entry)
XX
Pathogenic organism detection method associated DNA sequence #5.
DE
XX
KW Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
KW AIDS; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200277281-A1.
XX
PD 03-OCT-2002.
XX
PF 05-MAR-2002; 2002WO-JP002030.
XX
PR 27-MAR-2001; 2001JP-00090053.
PR 18-SEP-2001; 2001JP-00284112.
XX
(TOKE) TOSHIBA KK.
PA Hashimoto K, Hashimoto M, Mishihiro S, Oota Y;
PI Hashimoto K, Hashimoto M, Mishihiro S, Oota Y;
XX
WPI; 2003-040593/03.

CC This invention relates to a method for obtaining first data on a nucleic
CC acid from an individual exposed to a specific disease and second data on
CC a nucleic acid from a pathogenic microorganism occurring in the
CC individual in order to relate the specific disease to such pathogenic
CC microorganism. The method of the invention comprises the reaction of a
CC nucleic acid extract from the individual with a probe-immobilization
CC substrate containing first and second probes for detection of the
CC pathogenic microorganism with the first probe to relate to the specific
CC microbe-caused disease, and the second probe for detecting a specific
CC nucleic acid in the individual and obtaining first data from the reaction
CC probe and/or second data from the detected binding of a nucleic acid with
CC the second probe. The method of the invention is useful for detecting
CC nucleic acids relating diseases particularly due to pathogenic
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
CC also for therapeutic evaluation. Such a method is convenient and accurate
CC and may be used to design specific therapy for effective treatment even
CC for individual patients in a tailor-made manner. The present sequence
CC represents a nucleic acid sequence used in the scope of the invention
XX
SQ Sequence 581 BP; 118 A; 147 C; 214 G; 101 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 10; Length 581;

Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGTCTGTAGTGGCGGG 21
DB 410 GCAAGTCTGTAGTGGCGGG 430
|||||
RESULT 2
ABX08682
ID ABX08682 standard; DNA; 581 BP.
XX
AC ABX08682;
XX
DT 20-JAN-2003 (first entry)
XX
Pathogenic organism detection method associated DNA sequence #1.
DE
XX
KW Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
KW AIDS; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200277281-A1.
XX
PD 03-OCT-2002.
XX
PF 05-MAR-2002; 2002WO-JP002030.
XX
PR 27-MAR-2001; 2001JP-00090053.
PR 18-SEP-2001; 2001JP-00284112.
XX
(TOKE) TOSHIBA KK.
PA Hashimoto K, Hashimoto M, Mishihiro S, Oota Y;
PI Hashimoto K, Hashimoto M, Mishihiro S, Oota Y;
XX
WPI; 2003-040593/03.
XX
Detecting nucleic acids relating diseases particularly due to pathogenic
XX microorganisms e.g. hepatitis, influenza and AIDS in individuals from
XX their data using immobilized probes on substrate, also for therapeutic
XX evaluation.
XX
Claim 15; Page 87; 125pp; Japanese.
PS This invention relates to a method for obtaining first data on a nucleic
XX acid from an individual exposed to a specific disease and second data on
XX a nucleic acid from a pathogenic microorganism occurring in the
XX individual in order to relate the specific disease to such pathogenic
XX microorganism. The method of the invention comprises the reaction of a
XX nucleic acid extract from the individual with a probe-immobilization
XX substrate containing first and second probes for detection of the
XX pathogenic microorganism with the first probe to relate to the specific
XX microbe-caused disease, and the second probe for detecting a specific
XX nucleic acid in the individual and obtaining first data from the reaction
XX probe and/or second data from the detected binding of a nucleic acid with
XX the second probe. The method of the invention is useful for detecting
XX nucleic acids relating diseases particularly due to pathogenic
XX microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
XX also for therapeutic evaluation. Such a method is convenient and accurate
XX and may be used to design specific therapy for effective treatment even
XX for individual patients in a tailor-made manner. The present sequence
XX represents a nucleic acid sequence used in the scope of the invention
XX
SQ Sequence 581 BP; 118 A; 147 C; 214 G; 101 T; 0 U; 1 Other;
Query Match 95.2%; Score 20; DB 10; Length 581;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCTGTAGTGGCGGG 21
|||||

```
Db          410 GCAAGTGTGAGTGGCGGG 430
RESULT 3
ABX08685
ID ABX08685 standard; DNA; 581 BP.
XX
AC ABX08685;
XX
DT 20-JAN-2003 (first entry)
XX
DE Pathogenic organism detection method associated DNA sequence #4.
XX
KW Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
KW AIDS; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200277281-A1.
XX
PD 03-OCT-2002.
XX
PF 05-MAR-2002; 2002WO-JP002030.
XX
PR 27-MAR-2001; 2001JP-00090053.
PR 18-SEP-2001; 2001JP-00284112.
XX
PA (TOKE ) TOSHIBA KK.
XX
PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;
XX
DR WPI; 2003-040593/03.
XX
PT Detecting nucleic acids relating diseases particularly due to pathogenic
PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from
PT their data using immobilized probes on substrate, also for therapeutic
PT evaluation.
XX
PS Claim 15; Page 89; 125pp; Japanese.
XX
CC This invention relates to a method for obtaining first data on a nucleic
CC acid from an individual exposed to a specific disease and second data on
CC a nucleic acid from a pathogenic microorganism occurring in the
CC individual in order to relate the specific disease to such pathogenic
CC microorganism. The method of the invention comprises the reaction of a
CC nucleic acid extract from the individual with a probe-immobilization
CC substrate containing first and second probes for detection of the
CC pathogenic microorganism with the first probe to relate to the specific
CC nucleic acid in the individual and obtaining first data from the reaction
CC results as well as the detected binding of a nucleic acid with the first
CC probe and/or second data from the detected binding of a nucleic acid with
CC the second probe. The method of the invention is useful for detecting
CC nucleic acids relating diseases particularly due to pathogenic
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
CC also for therapeutic evaluation. Such a method is convenient and accurate
CC and may be used to design specific therapy for effective treatment even
CC for individual patients in a tailor-made manner. The present sequence
CC represents a nucleic acid sequence used in the scope of the invention
XX
SQ Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;
Query Match 95.2%; Score 20; DB 10; Length 581;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTGAGTGGCGGG 21
|||||
Db 410 GCAAGTGTGAGTGGCGGG 430
RESULT 4
ABX08684
ID ABX08684 standard; DNA; 581 BP.
XX
AC ABX08684;
XX
DT 20-JAN-2003 (first entry)
XX
DE Pathogenic organism detection method associated DNA sequence #2.
XX
KW Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
KW AIDS; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200277281-A1.
XX
PD 03-OCT-2002.
XX
PF 05-MAR-2002; 2002WO-JP002030.
XX
PR 27-MAR-2001; 2001JP-00090053.
PR 18-SEP-2001; 2001JP-00284112.
XX
PA (TOKE ) TOSHIBA KK.
XX
PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;
XX
DR WPI; 2003-040593/03.
XX
PT Detecting nucleic acids relating diseases particularly due to pathogenic
PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from
PT their data using immobilized probes on substrate, also for therapeutic
PT evaluation.
XX
PS Claim 15; Page 88; 125pp; Japanese.
XX
CC This invention relates to a method for obtaining first data on a nucleic
CC acid from an individual exposed to a specific disease and second data on
CC a nucleic acid from a pathogenic microorganism occurring in the
CC individual in order to relate the specific disease to such pathogenic
CC microorganism. The method of the invention comprises the reaction of a
CC nucleic acid extract from the individual with a probe-immobilization
CC substrate containing first and second probes for detection of the
CC pathogenic microorganism with the first probe to relate to the specific
CC nucleic acid in the individual and obtaining first data from the reaction
CC results as well as the detected binding of a nucleic acid with the first
CC probe and/or second data from the detected binding of a nucleic acid with
CC the second probe. The method of the invention is useful for detecting
CC nucleic acids relating diseases particularly due to pathogenic
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
CC also for therapeutic evaluation. Such a method is convenient and accurate
CC and may be used to design specific therapy for effective treatment even
CC for individual patients in a tailor-made manner. The present sequence
CC represents a nucleic acid sequence used in the scope of the invention
XX
SQ Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;
Query Match 95.2%; Score 20; DB 10; Length 581;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTGAGTGGCGGG 21
|||||
Db 410 GCAAGTGTGAGTGGCGGG 430
RESULT 5
ABX08684
ID ABX08684 standard; DNA; 581 BP.
XX
AC ABX08684;
XX
DT 20-JAN-2003 (first entry)
```

XX DE Pathogenic organism detection method associated DNA sequence #3.
XX DE Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
KW AIDS; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX WO200277281-A1.
XX PN 03-OCT-2002.
XX PD 05-MAR-2002; 2002WO-JP002030.
XX PF 27-MAR-2001; 2001JP-00090053.
XX PR 18-SEP-2001; 2001JP-00284112.
XX PA (TOKE) TOSHIBA KK.
XX PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;
XX WPI; 2003-040593/03.
XX DR
XX PT Detecting nucleic acids relating diseases particularly due to pathogenic
PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from
PT their data using immobilized probes on substrate, also for therapeutic
PT evaluation.
XX PS Claim 15; Page 88; 125pp; Japanese.
XX SQ
CC This invention relates to a method for obtaining first data on a nucleic
CC acid from an individual exposed to a specific disease and second data on
CC a nucleic acid from a pathogenic microorganism occurring in the
CC individual in order to relate the specific disease to such pathogenic
CC microorganism. The method of the invention comprises the reaction of a
CC nucleic acid extract from the individual with a probe-immobilization
CC substrate containing first and second probes for detection of the
CC pathogenic microorganism with the first probe to relate to the specific
CC nucleic acid in the individual and the second probe for detecting a specific
CC results as well as the detected binding of a nucleic acid with the first
CC probe and/or second data from the detected binding of a nucleic acid with
CC the second probe. The method of the invention is useful for detecting
CC nucleic acids relating diseases particularly due to pathogenic
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
CC also for therapeutic evaluation. Such a method is convenient and accurate
CC and may be used to design specific therapy for effective treatment even
CC for individual patients in a tailor-made manner. The present sequence
CC represents a nucleic acid sequence used in the scope of the invention
XX SQ Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;
Query Match 95.2%; Score 20; DB 10; Length 581;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCTGTAGTGGGGG 21
Db 410 GCAAGTCTGNAGTGGGGG 430
RESULT 6
ADL92264
ID ADL92264 standard; DNA; 581 BP.
XX AC ADL92264;
XX DT 20-MAY-2004 (first entry)
XX DE Human MxA gene DNA sequence #2.
XX KW nucleic acid detection; immobilised nucleic acid probe;
KW single nucleotide polymorphism detection; SNP detection;
KW
XX

KW disease diagnosis; ds; human; MxA gene.
XX OS Homo sapiens.
XX PN JP2004041109-A.
XX PD 12-FEB-2004.
XX PF 12-JUL-2002; 2002JP-00204444.
XX PR 12-JUL-2002; 2002JP-00204444.
XX PA (TOKE) TOSHIBA KK.
XX DR WPI; 2004-151026/15.
XX PT Detecting target nucleic acid (T) using probe, comprises amplifying
PT target sequence (S) so that end of (S) which is hybridized with probe is
PT positioned at less than 40 bases from terminal base of (T) and detecting
PT hybridization with probe.
XX PS Disclosure; SEQ ID NO 21; 47pp; Japanese.
XX SQ Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;
Query Match 95.2%; Score 20; DB 12; Length 581;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCTGTAGTGGGGG 21
Db 410 GCAAGTCTGNAGTGGGGG 430
RESULT 7
ADL92256
ID ADL92256 standard; DNA; 46 BP.
XX AC ADL92256;
XX DT 20-MAY-2004 (first entry)
XX DE Human MxA gene PCR primer #2.
XX KW nucleic acid detection; immobilised nucleic acid probe;
KW single nucleotide polymorphism detection; SNP detection;
KW disease diagnosis; PCR; primer; ss; human; MxA gene.
XX OS Homo sapiens.
XX PN JP2004041109-A.
XX PD 12-FEB-2004.
XX PF 12-JUL-2002; 2002JP-00204444.
XX PR 12-JUL-2002; 2002JP-00204444.
XX PA (TOKE) TOSHIBA KK.
XX DR WPI; 2004-151026/15.
XX PT Detecting target nucleic acid (T) using probe, comprises amplifying
PT target sequence (S) so that end of (S) which is hybridized with probe is
PT positioned at less than 40 bases from terminal base of (T) and detecting
PT


```
PT hybridization with probe.
XX
PS Claim 6; SEQ ID NO 13; 47bp; Japanese.
XX
CC The invention comprises a method for detecting a target nucleic acid. The
CC method of the invention is useful for: single nucleotide polymorphism
CC detection, diagnosis of disease by analysing disease-related genes,
CC estimating risk of incidence of the disease, detection of infection,
CC analysing virus types, and in toxicity studies. The present DNA sequence
CC represents a PCR primer of the invention.
XX
SQ Sequence 46 BP; 7 A; 9 C; 19 G; 11 T; 0 U; 0 Other;

Query Match          92.4%; Score 19.4; DB 12; Length 46;
Best Local Similarity 95.2%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db ||||||||| |||||||||
4 GCAAGTGTCTGACAGGTGCGGG 24

RESULT 8
ADO78057/c
ID ADO78057 standard; DNA; 132 BP.
XX
AC ADO78057;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human MxA gene promoter region #2.
XX
KW nucleic acid analysis; single nucleotide polymorphism detection;
KW SNP detection; human; MxA; promoter; ds.
XX
OS Homo sapiens.
XX
PN JP2004121044-A.
XX
PD 22-APR-2004.
XX
PF 30-SEP-2002; 2002JP-00287376.
XX
PR 30-SEP-2002; 2002JP-00287376.
XX
PA (TOKE ) TOSHIBA KK.
XX
WPI; 2004-322749/30.
XX
DE Human MxA gene promoter region #2.
XX
KW nucleic acid analysis; single nucleotide polymorphism detection;
KW SNP detection; human; MxA; promoter; ds.
XX
OS Homo sapiens.
XX
PN JP2004121044-A.
XX
PD 22-APR-2004.
XX
PF 30-SEP-2002; 2002JP-00287376.
XX
PR 30-SEP-2002; 2002JP-00287376.
XX
PA (TOKE ) TOSHIBA KK.
XX
WPI; 2004-322749/30.
XX
DE Analyzing nucleic acid sequence, involves allowing nucleic acid in sample
PT to react and hybridize with first and second probe having homologous
PT sequence except for single base at target region.
XX
PS Example 1; SEQ ID NO 2; 16pp; Japanese.
XX
CC The invention comprises a method for analysing a nucleic acid sequence,
CC the method involves allowing the nucleic acid in a sample to hybridise
CC with a first probe and a second probe which is shorter than the first
CC probe by one base, where the sequence of the first and second probe are
CC homologous except for a single base at the target region. The method of
CC the invention is useful for analysing nucleic acid sequences (e.g. single
CC nucleotide polymorphism detection). The present DNA sequence represents a
CC region of the human MxA gene promoter which was used in an example of the
CC invention.
XX
SQ Sequence 132 BP; 22 A; 46 C; 38 G; 26 T; 0 U; 0 Other;

Query Match          92.4%; Score 19.4; DB 12; Length 132;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||
```

```
FT misc_feature 441..456
FT /*tag= a
FT /function= "interferon-stimulated response element"
FT variation
FT replace(455,V)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX
XX PN EP1136571-A2.
XX
XX PD 26-SEP-2001.
XX
XX PF 22-MAR-2001; 2001EP-00302708.
XX
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062371.
XX
XX PA (TOKE ) TOSHIBA KK.
XX
XX PI Hijikata M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640393/74.
XX
XX DR New polynucleotides, useful for predicting validity of interferon in
XX individual infected with hepatitis C virus and in gene therapy for
XX PT interferon therapy, comprises polymorphisms in MxA gene.
XX
XX PS Claim 1; Page 13; 25pp; English.
XX
XX CC The present sequence is that of the promoter region of the human MxA
XX gene. The promoter includes an interferon-stimulated response element
XX (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
XX ISRE affects the sensitivity of an individual to interferon therapy. The
XX therapy is valid when the SNP nucleotide is thymine and invalid when the
XX SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
XX the nucleotide at the SNP site is thymine. Polynucleotides of the
XX invention, which comprise the MxA promoter having thymine, guanine,
XX adenine or cytosine at the SNP site, or which comprise the corresponding
XX ISRE, modified or complementary polynucleotides, can be used to predict
XX the validity of interferon therapy for an individual, especially an
XX individual infected with hepatitis C virus (claimed). The polynucleotide
XX which has thymine at the SNP site can also be used in gene therapy, to
XX render an interferon-insensitive individual to be interferon-sensitive
XX (also claimed)
XX
XX SQ Sequence 581 BP; 118 A; 147 C; 214 G; 101 T; 0 U; 1 Other;
XX
XX Query Match 92.4%; Score 19.4; DB 4; Length 581;
XX Best Local Similarity 95.2%; Pred. No. 41;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCAAGTGCTGTAGGTGCGGGG 21
XX ||||| ||||| ||||| |||||
XX Db 410 GCAAGTGCTGTAGGTGCGGGG 430
XX
XX RESULT 11
XX AAI70375
XX ID AAI70375 standard; DNA; 581 BP.
XX
XX AC AAI70375;
XX
XX DT 07-JAN-2002 (first entry)
XX
XX DE Human MxA gene promoter region (adenine variant).
XX
XX KW MxA gene; human; promoter; interferon; therapy; hepatitis C virus;
XX polymorphism; gene therapy; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX misc_feature 441..456
XX /*tag= a
XX FT variation
XX replace(455,D)
```

```
FT variation
FT replace(455,B)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX
XX PN EP1136571-A2.
XX
XX PD 26-SEP-2001.
XX
XX PF 22-MAR-2001; 2001EP-00302708.
XX
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062371.
XX
XX PA (TOKE ) TOSHIBA KK.
XX
XX PI Hijikata M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640393/74.
XX
XX DR New polynucleotides, useful for predicting validity of interferon in
XX individual infected with hepatitis C virus and in gene therapy for
XX PT interferon therapy, comprises polymorphisms in MxA gene.
XX
XX PS Claim 3; Page 14; 25pp; English.
XX
XX CC The present sequence is that of the promoter region of the human MxA
XX gene. The promoter includes an interferon-stimulated response element
XX (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
XX ISRE affects the sensitivity of an individual to interferon therapy. The
XX therapy is valid when the SNP nucleotide is thymine and invalid when the
XX SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
XX the nucleotide at the SNP site is adenine. Polynucleotides of the
XX invention, which comprise the MxA promoter having thymine, guanine,
XX adenine or cytosine at the SNP site, or which comprise the corresponding
XX ISRE, modified or complementary polynucleotides, can be used to predict
XX the validity of interferon therapy for an individual, especially an
XX individual infected with hepatitis C virus (claimed). The polynucleotide
XX which has thymine at the SNP site (see AAI70373) can also be used in gene
XX therapy, to render an interferon-insensitive individual to be interferon-
XX sensitive (also claimed)
XX
XX SQ Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;
XX
XX Query Match 92.4%; Score 19.4; DB 4; Length 581;
XX Best Local Similarity 95.2%; Pred. No. 41;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCAAGTGCTGTAGGTGCGGGG 21
XX ||||| ||||| ||||| |||||
XX Db 410 GCAAGTGCTGTAGGTGCGGGG 430
XX
XX RESULT 12
XX AAI70376
XX ID AAI70376 standard; DNA; 581 BP.
XX
XX AC AAI70376;
XX
XX DT 07-JAN-2002 (first entry)
XX
XX DE Human MxA gene promoter region (cytosine variant).
XX
XX KW MxA gene; human; promoter; interferon; therapy; hepatitis C virus;
XX polymorphism; gene therapy; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX misc_feature 441..456
XX /*tag= a
XX /function= "interferon-stimulated response element"
XX FT variation
XX replace(455,D)
```

```

FT FT /*tag= b
XX XX /standard_name= "single nucleotide polymorphism"
PN PN
XX XX
PD PD
XX XX
XX XX
PF PF 22-MAR-2001; 2001EP-00302708.
XX XX
XX XX 22-MAR-2000; 2000JP-00080955.
PR PR 06-MAR-2001; 2001JP-00062371.
XX XX
XX XX (TOKE ) TOSHIBA KK.
PA PA
XX XX
PI PI Hijikata M, Mishihiro S, Oota Y, Hashimoto K;
XX XX
XX XX WPI; 2001-640393/74.
DR DR
XX XX
XX XX New polynucleotides, useful for predicting validity of interferon in
PT PT individual infected with hepatitis C virus and in gene therapy for
PT PT interferon therapy, comprises polymorphisms in MxA gene.
XX XX
PS PS Claim 3; Page 14; 25pp; English.
XX XX
CC CC The present sequence is that of the promoter region of the human MxA
CC CC gene. The promoter includes an interferon-stimulated response element
CC CC (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
CC CC ISRE affects the sensitivity of an individual to interferon therapy. The
CC CC therapy is valid when the SNP nucleotide is thymine and invalid when the
CC CC SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
CC CC the nucleotide at the SNP site is cytosine. Polynucleotides of the
CC CC invention, which comprise the MxA promoter having thymine, guanine,
CC CC adenine or cytosine at the SNP site, or which comprise the corresponding
CC CC ISRE, modified or complementary polynucleotides, can be used to predict
CC CC the validity of interferon therapy for an individual, especially an
CC CC individual infected with hepatitis C virus (claimed). The polynucleotide
CC CC which has thymine at the SNP site (see AAI70373) can also be used in gene
CC CC therapy, to render an interferon-insensitive individual to be interferon-
CC CC sensitive (also claimed)
XX XX
SQ Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 4; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGAGTGCGGGG 21
Db ||||||| |||||||
410 GCAAGTGTCTGAGTGCGGGG 430

RESULT 13
AAI70374
ID AAI70374 standard; DNA; 581 BP.
XX XX
AC AAI70374;
XX XX
DT 07-JAN-2002 (first entry)
XX XX
DE Human MxA gene promoter region (guanine variant).
XX XX
XX MxA gene; human; promoter; interferon; therapy; hepatitis C virus;
KW polymorphism; gene therapy; ds.
XX XX
OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
FH misc_feature 441..456
FT /*tag= a
FT /function= "interferon-stimulated response element"
FT variation replace(455,H)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
FT FT

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```

XX XX EP1136571-A2.
PN PN
XX XX
PD PD
XX XX
XX XX 26-SEP-2001.
PF PF
XX XX 22-MAR-2001; 2001EP-00302708.
XX XX
XX XX 22-MAR-2000; 2000JP-00080955.
PR PR 06-MAR-2001; 2001JP-00062371.
XX XX
XX XX (TOKE ) TOSHIBA KK.
PA PA
XX XX
PI PI Hijikata M, Mishihiro S, Oota Y, Hashimoto K;
XX XX
XX XX WPI; 2001-640393/74.
DR DR
XX XX
XX XX New polynucleotides, useful for predicting validity of interferon in
PT PT individual infected with hepatitis C virus and in gene therapy for
PT PT interferon therapy, comprises polymorphisms in MxA gene.
XX XX
PS PS Claim 2; Page 14; 25pp; English.
XX XX
CC CC The present sequence is that of the promoter region of the human MxA
CC CC gene. The promoter includes an interferon-stimulated response element
CC CC (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
CC CC ISRE affects the sensitivity of an individual to interferon therapy. The
CC CC therapy is valid when the SNP nucleotide is thymine and invalid when the
CC CC SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
CC CC the nucleotide at the SNP site is guanine. Polynucleotides of the
CC CC invention, which comprise the MxA promoter having thymine, guanine,
CC CC adenine or cytosine at the SNP site, or which comprise the corresponding
CC CC ISRE, modified or complementary polynucleotides, can be used to predict
CC CC the validity of interferon therapy for an individual, especially an
CC CC individual infected with hepatitis C virus (claimed). The polynucleotide
CC CC which has thymine at the SNP site (see AAI70373) can also be used in gene
CC CC therapy, to render an interferon-insensitive individual to be interferon-
CC CC sensitive (also claimed)
XX XX
SQ Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 4; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGAGTGCGGGG 21
Db ||||||| |||||||
410 GCAAGTGTCTGAGTGCGGGG 430

RESULT 14
AAI70353
ID AAI70353 standard; DNA; 581 BP.
XX XX
AC AAI70353;
XX XX
DT 07-JAN-2002 (first entry)
XX XX
DE Promoter region of human MxA gene (C at position 455).
XX XX
XX MxA gene; human; promoter; interferon; therapy; validation;
KW gene detection; hepatitis C virus; DNA chip; ds.
XX XX
OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
FH misc_feature 441..456
FT /*tag= a
FT /function= "interferon-stimulated response element"
FT variation replace(455,D)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
FT FT
PN EP1136570-A2.

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XX PD 26-SEP-2001.
XX PF
XX PF 22-MAR-2001; 2001EP-00302705.
XX PR
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062372.
XX PA (TOKE ) TOSHIBA KK.
XX PI
XX PI Hijitaka M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640392/74.
XX
XX New carriers for gene detection, particularly useful for detecting
PT validity of interferon therapy, especially in a patient infected with
PT hepatitis C virus.
XX
XX Claim 4; Page 19; 33pp; English.
XX
XX The present sequence is that of the promoter region of the human MxA
CC gene, in which the 15th position of an interferon-stimulated response
CC element (ISRE) is cytosine. A single nucleotide polymorphism (SNP) at
CC this site affects the sensitivity of an individual to interferon therapy.
CC Interferon therapy is less effective for individuals having an ISRE which
CC is not either T/T homozygous or T/non-T heterozygous at this site. Use of
CC carriers for gene detection of the present invention allows examination
CC of whether the SNP site in the MxA gene promoter from a subject is
CC thymine or not. The method uses a carrier for gene detection comprising a
CC base body onto which a polynucleotide is immobilized. The polynucleotide
CC may comprise the present sequence, a modified polynucleotide derived from
CC it, a polynucleotide spanning positions 441-455 or positions 449-459, or
CC a polynucleotide complementary to any of these. A DNA chip for use in
CC gene detection is also claimed. Detection of hybridisation with a
CC polynucleotide taken e.g. from a hepatitis C virus-infected individual
CC may be carried out by detecting an electrochemical change that
CC accompanies hybridisation
XX
XX Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;
SQ
Query Match 92.4%; Score 19.4; DB 5; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCAAGTGCTGCTAGGTCGCGGG 21
Db 410 GCAAGTGCTGCTAGGTCGCGGG 430
RESULT 15
AAI70350
ID AAI70350 standard; DNA; 581 BP.
XX
XX AAI70350;
XX
XX 07-JAN-2002 (first entry)
XX
XX Promoter region of human MxA gene (T at position 455).
XX
XX MxA gene; human; promoter; interferon; therapy; validation;
KW gene detection; hepatitis C virus; DNA chip; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 441..456
FT /*tag= a
FT /function= "interferon-stimulated response element"
FT replace(455,v)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX
XX EPI136570-A2.

```

```

XX PD 26-SEP-2001.
XX PF
XX PF 22-MAR-2001; 2001EP-00302705.
XX PR
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062372.
XX PA (TOKE ) TOSHIBA KK.
XX PI
XX PI Hijitaka M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640392/74.
XX
XX New carriers for gene detection, particularly useful for detecting
PT validity of interferon therapy, especially in a patient infected with
PT hepatitis C virus.
XX
XX Claim 1; Page 18; 33pp; English.
XX
XX The present sequence is that of the promoter region of the human MxA
CC gene, in which the 15th position of an interferon-stimulated response
CC element (ISRE) is thymine. A single nucleotide polymorphism (SNP) at this
CC site affects the sensitivity of an individual to interferon therapy.
CC Interferon therapy is more effective for individuals having an ISRE which
CC is either T/T homozygous or T/non-T heterozygous at this site. Use of
CC carriers for gene detection of the present invention allows examination
CC of whether the SNP site in the MxA gene promoter from a subject is
CC thymine or not. The method uses a carrier for gene detection comprising a
CC base body onto which a polynucleotide is immobilized. The polynucleotide
CC may comprise the present sequence, a modified polynucleotide derived from
CC it, a polynucleotide spanning positions 441-455 or positions 449-459, or
CC a polynucleotide complementary to any of these. A DNA chip is also
CC claimed. Detection of hybridisation with a polynucleotide taken e.g. from
CC a hepatitis C virus-infected individual may be carried out by detecting
CC an electrochemical change that accompanies the hybridisation
XX
XX Sequence 581 BP; 118 A; 147 C; 214 G; 101 T; 0 U; 1 Other;
SQ
Query Match 92.4%; Score 19.4; DB 5; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCAAGTGCTGCTAGGTCGCGGG 21
Db 410 GCAAGTGCTGCTAGGTCGCGGG 430
RESULT 16
AAI70352
ID AAI70352 standard; DNA; 581 BP.
XX
XX AAI70352;
XX
XX 07-JAN-2002 (first entry)
XX
XX Promoter region of human MxA gene (A at position 455).
XX
XX MxA gene; human; promoter; interferon; therapy; validation;
KW gene detection; hepatitis C virus; DNA chip; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 441..456
FT /*tag= a
FT /function= "interferon-stimulated response element"
FT replace(455,B)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX
XX EPI136570-A2.

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PD 26-SEP-2001.
XX PF
XX 22-MAR-2001; 2001EP-00302705.
XX PR
XX 22-MAR-2000; 2000JP-00080955.
XX PR
XX 06-MAR-2001; 2001JP-00062372.
XX PR
XX (TOKE ) TOSHIBA KK.
XX PA
XX
XX Hijitaka M, Mishihiro S, Oota Y, Hashimoto K;
XX PI
XX WPI; 2001-640392/74.
XX DR
XX
XX New carriers for gene detection, particularly useful for detecting
PT validity of interferon therapy, especially in a patient infected with
PT hepatitis C virus.
XX PT
XX
XX Claim 3; Page 19; 33pp; English.
XX PS
XX
XX The present sequence is that of the promoter region of the human MxA
CC gene, in which the 15th position of an interferon-stimulated response
CC element (ISRE) is adenine. A single nucleotide polymorphism (SNP) at this
CC site affects the sensitivity of an individual to interferon therapy.
CC Interferon therapy is less effective for individuals having an ISRE which
CC is not either T/T homozygous or T/non-T heterozygous at this site. Use of
CC carriers for gene detection of the present invention allows examination
CC of whether the SNP site in the MxA gene promoter from a subject is
CC thymine or not. The method uses a carrier for gene detection comprising a
CC base body onto which a polynucleotide is immobilized. The polynucleotide
CC may comprise the present sequence, a modified polynucleotide derived from
CC it, a polynucleotide spanning positions 441-455 or positions 449-459, or
CC a polynucleotide complementary to any of these. A DNA chip for use in
CC gene detection is also claimed. Detection of hybridisation with a
CC polynucleotide taken from the individual may be carried out by detecting
CC an electrochemical change that accompanies the hybridisation
XX
XX Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;
SQ
Query Match 92.4%; Score 19.4; DB 5; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGTAGTGGCGGG 21
DB 410 GCAAGTGTCTGTAGTGGCGGG 430

RESULT 17
AAI70351
XX ID AAI70351 standard; DNA; 581 BP.
XX AC
XX AAI70351;
XX DT
XX 07-JAN-2002 (first entry)
XX DE
XX Promoter region of human MxA gene (G at position 455).
XX MxA gene; human; promoter; interferon; therapy; validation;
XX gene detection; hepatitis C virus; DNA chip; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX misc_feature 441..456
XX /*tag= a
XX /function= "interferon-stimulated response element";
XX variation replace(455,H)
XX /*tag= b
XX /standard_name= "single nucleotide polymorphism"
XX EP1136570-A2.
XX PN
XX 26-SEP-2001.
XX PD

XX 22-MAR-2001; 2001EP-00302705.
XX PF
XX 22-MAR-2000; 2000JP-00080955.
XX PR
XX 06-MAR-2001; 2001JP-00062372.
XX PR
XX (TOKE ) TOSHIBA KK.
XX PA
XX
XX Hijitaka M, Mishihiro S, Oota Y, Hashimoto K;
XX PI
XX WPI; 2001-640392/74.
XX DR
XX
XX New carriers for gene detection, particularly useful for detecting
PT validity of interferon therapy, especially in a patient infected with
PT hepatitis C virus.
XX PT
XX
XX Claim 2; Page 19; 33pp; English.
XX PS
XX
XX The present sequence is that of the promoter region of the human MxA
CC gene, in which the 15th position of an interferon-stimulated response
CC element (ISRE) is guanine. A single nucleotide polymorphism (SNP) at this
CC site affects the sensitivity of an individual to interferon therapy.
CC Interferon therapy is less effective for individuals having an ISRE which
CC is not either T/T homozygous or T/non-T heterozygous at this site. Use of
CC carriers for gene detection of the present invention allows examination
CC of whether the SNP site in the MxA gene promoter from a subject is
CC thymine or not. The method uses a carrier for gene detection comprising a
CC base body onto which a polynucleotide is immobilized. The polynucleotide
CC may comprise the present sequence, a modified polynucleotide derived from
CC it, a polynucleotide spanning positions 441-455 or positions 449-459, or
CC a polynucleotide complementary to any of these. A DNA chip is also
CC claimed. Detection of hybridisation with a polynucleotide taken e.g. from
CC a hepatitis C virus-infected individual may be carried out by detecting
CC an electrochemical change that accompanies hybridisation
XX
XX Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;
SQ
Query Match 92.4%; Score 19.4; DB 5; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTGTAGTGGCGGG 21
DB 410 GCAAGTGTCTGTAGTGGCGGG 430

RESULT 18
ABX08706
XX ID ABX08706 standard; DNA; 581 BP.
XX AC
XX ABX08706;
XX DT
XX 20-JAN-2003 (first entry)
XX DE
XX Pathogenic organism detection method associated DNA sequence #8.
XX Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
XX AIDS; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX WO200277281-A1.
XX PN
XX 03-OCT-2002.
XX PD
XX
XX 05-MAR-2002; 2002WO-JP002030.
XX PF
XX 27-MAR-2001; 2001JP-00090053.
XX PR
XX 18-SEP-2001; 2001JP-00284112.
XX PR
XX (TOKE ) TOSHIBA KK.
XX PA
XX Hashimoto K, Hashimoto M, Mishihiro S, Oota Y;
XX PI

```

XX WPI; 2003-040593/03.

XX Detecting nucleic acids relating diseases particularly due to pathogenic

XX microorganisms e.g. hepatitis, influenza and AIDS in individuals from

PT their data using immobilized probes on substrate, also for therapeutic

PT evaluation.

XX Claim 15; Page 95; 125pp; Japanese.

XX This invention relates to a method for obtaining first data on a nucleic

XX acid from an individual exposed to a specific disease and second data on

CC a nucleic acid from a pathogenic microorganism occurring in the

CC individual in order to relate the specific disease to such pathogenic

CC microorganism. The method of the invention comprises the reaction of a

CC nucleic acid extract from the individual with a probe-immobilization

CC substrate containing first and second probes for detection of the

CC pathogenic microorganism with the first probe to relate to the specific

CC microbe-caused disease, and the second probe for detecting a specific

CC nucleic acid in the individual and obtaining first data from the reaction

CC probe and/or second data from the detected binding of a nucleic acid with

CC the second probe. The method of the invention is useful for detecting

CC nucleic acids relating diseases particularly due to pathogenic

CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and

CC also for therapeutic evaluation. Such a method is convenient and accurate

CC and may be used to design specific therapy for effective treatment even

CC for individual patients in a tailor-made manner. The present sequence

CC represents a nucleic acid sequence used in the scope of the invention

XX Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;

SQ

Query Match 92.4%; Score 19.4; DB 10; Length 581;

Best Local Similarity 95.2%; Pred. No. 41;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGG 21

DB 410 GCAAGTGTCTAGTGGGG 430

RESULT 19

ABX08704

ID ABX08704 standard; DNA; 581 BP.

XX AC ABX08704;

XX DT 20-JAN-2003 (first entry)

XX Pathogenic organism detection method associated DNA sequence #6.

XX Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;

XX AIDS; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200277281-A1.

XX 03-OCT-2002.

XX 05-MAR-2002; 2002WO-JP002030.

XX 27-MAR-2001; 2001JP-00090053.

XX 18-SEP-2001; 2001JP-00284112.

XX (TOKE) TOSHIBA KK.

XX Hashimoto K, Hashimoto M, Mishiro S, Oota Y;

XX WPI; 2003-040593/03.

XX Detecting nucleic acids relating diseases particularly due to pathogenic

PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from

PT their data using immobilized probes on substrate, also for therapeutic

PT evaluation.

XX Claim 15; Page 94; 125pp; Japanese.

XX This invention relates to a method for obtaining first data on a nucleic

XX acid from an individual exposed to a specific disease and second data on

CC a nucleic acid from a pathogenic microorganism occurring in the

CC individual in order to relate the specific disease to such pathogenic

CC microorganism. The method of the invention comprises the reaction of a

CC nucleic acid extract from the individual with a probe-immobilization

CC substrate containing first and second probes for detection of the

CC pathogenic microorganism with the first probe to relate to the specific

CC microbe-caused disease, and the second probe for detecting a specific

CC nucleic acid in the individual and obtaining first data from the reaction

CC probe and/or second data from the detected binding of a nucleic acid with

CC the second probe. The method of the invention is useful for detecting

CC nucleic acids relating diseases particularly due to pathogenic

CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and

CC also for therapeutic evaluation. Such a method is convenient and accurate

CC and may be used to design specific therapy for effective treatment even

CC for individual patients in a tailor-made manner. The present sequence

CC represents a nucleic acid sequence used in the scope of the invention

XX Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;

SQ

Query Match 92.4%; Score 19.4; DB 10; Length 581;

Best Local Similarity 95.2%; Pred. No. 41;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGGG 21

DB 410 GCAAGTGTCTAGTGGGG 430

RESULT 20

ABX08705

ID ABX08705 standard; DNA; 581 BP.

XX AC ABX08705;

XX DT 20-JAN-2003 (first entry)

XX Pathogenic organism detection method associated DNA sequence #7.

XX Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;

XX AIDS; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200277281-A1.

XX 03-OCT-2002.

XX 05-MAR-2002; 2002WO-JP002030.

XX 27-MAR-2001; 2001JP-00090053.

XX 18-SEP-2001; 2001JP-00284112.

XX (TOKE) TOSHIBA KK.

XX Hashimoto K, Hashimoto M, Mishiro S, Oota Y;

XX WPI; 2003-040593/03.

XX Detecting nucleic acids relating diseases particularly due to pathogenic

PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from

PT their data using immobilized probes on substrate, also for therapeutic

PT evaluation.

XX Claim 15; Page 94-95; 125pp; Japanese.

CC This invention relates to a method for obtaining first data on a nucleic
CC acid from an individual exposed to a specific disease and second data on
CC a nucleic acid from a pathogenic microorganism occurring in the
CC individual in order to relate the specific disease to such pathogenic
CC microorganism. The method of the invention comprises the reaction of a
CC nucleic acid extract from the individual with a probe-immobilization
CC substrate containing first and second probes for detection of the
CC pathogenic microorganism with the first probe to relate to the specific
CC microbe-caused disease, and the second probe for detecting a specific
CC nucleic acid in the individual and obtaining first data from the reaction
CC results as well as the detected binding of a nucleic acid with the first
CC probe and/or second data from the detected binding of a nucleic acid with
CC the second probe. The method of the invention is useful for detecting
CC nucleic acids relating diseases particularly due to pathogenic
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
CC also for therapeutic evaluation. Such a method is convenient and accurate
CC and may be used to design specific therapy for effective treatment even
CC for individual patients in a tailor-made manner. The present sequence
CC represents a nucleic acid sequence used in the scope of the invention
XX

XX SQ Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 10; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 21

ADL92270
ID ADL92270 standard; DNA; 581 BP.

XX AC ADL92270;

XX DT 20-MAY-2004 (first entry)

XX DE Human MxA gene DNA sequence #8.

XX KW nucleic acid detection; immobilised nucleic acid probe;
KW single nucleotide polymorphism detection; SNP detection;
KW disease diagnosis; ds; human; MxA gene.

XX OS Homo sapiens.

XX PN JP2004041109-A.

XX PD 12-FEB-2004.

XX PF 12-JUL-2002; 2002JP-00204444.

XX PR 12-JUL-2002; 2002JP-00204444.

XX PA (TOKE) TOSHIBA KK.

XX DR WPI; 2004-151026/15.

XX PT Detecting target nucleic acid (T) using probe, comprises amplifying
PT target sequence (S) so that end of (S) which is hybridized with probe is
PT positioned at less than 40 bases from terminal base of (T) and detecting
PT hybridization with probe.

XX PS Disclosure; SEQ ID NO 27; 47pp; Japanese.

XX CC The invention comprises a method for detecting a target nucleic acid. The
CC method of the invention is useful for: single nucleotide polymorphism
CC detection, diagnosis of disease by analysing disease-related genes,
CC estimating risk of incidence of the disease, detection of infection,
CC analysing virus types, and in toxicity studies. The present nucleic acid
CC represents a human MxA gene DNA sequence which was used in the
CC exemplification of the invention.

XX SQ

Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 12; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 22

ADL92267
ID ADL92267 standard; DNA; 581 BP.

XX AC ADL92267;

XX DT 20-MAY-2004 (first entry)

XX DE Human MxA gene DNA sequence #5.

XX KW nucleic acid detection; immobilised nucleic acid probe;
KW single nucleotide polymorphism detection; SNP detection;
KW disease diagnosis; ds; human; MxA gene.

XX OS Homo sapiens.

XX PN JP2004041109-A.

XX PD 12-FEB-2004.

XX PF 12-JUL-2002; 2002JP-00204444.

XX PR 12-JUL-2002; 2002JP-00204444.

XX PA (TOKE) TOSHIBA KK.

XX DR WPI; 2004-151026/15.

XX PT Detecting target nucleic acid (T) using probe, comprises amplifying
PT target sequence (S) so that end of (S) which is hybridized with probe is
PT positioned at less than 40 bases from terminal base of (T) and detecting
PT hybridization with probe.

XX PS Disclosure; SEQ ID NO 24; 47pp; Japanese.

XX CC The invention comprises a method for detecting a target nucleic acid. The
CC method of the invention is useful for: single nucleotide polymorphism
CC detection, diagnosis of disease by analysing disease-related genes,
CC estimating risk of incidence of the disease, detection of infection,
CC analysing virus types, and in toxicity studies. The present nucleic acid
CC represents a human MxA gene DNA sequence which was used in the
CC exemplification of the invention.

XX SQ Sequence 581 BP; 119 A; 147 C; 213 G; 101 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 12; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
DB 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 23

AAD55993
ID AAD55993 standard; DNA; 2451 BP.

XX AC AAD55993;

XX DT 07-AUG-2003 (first entry)

XX Human MxA domain DNA.
 DE
 XX MxA; GTPase; cancer; gene therapy; cytostatic; human; gene; ds.
 KW
 XX Homo sapiens.
 OS
 XX WO2003033667-A2.
 PN
 XX 24-APR-2003.
 PD
 XX 18-OCT-2002; 2002WO-US033232.
 PF
 XX 18-OCT-2001; 2001US-0329740P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PA Mushinski FJ, Trepel JB, Horisberger MA, Nguyen P, Khanna C;
 PI
 XX WPI; 2003-393519/37.
 DR
 XX Use of a polypeptide having at least 90% amino acid sequence identity to
 PT human MxA or a nucleic acid encoding the protein in preparing a
 PT medicament for reducing cancer progression in a mammal.
 PT
 XX Disclosure; Page 57-58; 62pp; English.
 PS
 XX The invention relates to the use of a polypeptide having at least 90%
 CC amino acid sequence identity to human MxA or a nucleic acid encoding the
 CC protein. Mx proteins belong to a family of unique GTPases. The invention
 CC is used for preparing a medicament for reducing cancer progression in a
 CC mammal. It is also used in gene therapy. The present sequence is human
 CC MxA domain encoding DNA used in the invention
 CC
 XX Sequence 2451 BP; 591 A; 553 C; 704 G; 603 T; 0 U; 0 Other;
 SQ
 Query Match 92.4%; Score 19.4; DB 9; Length 2451;
 Best Local Similarity 95.2%; Pred. No. 46;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTCTGTAGTGGGGG 21
 DB 2398 GCAAGTCTGCAGGTGGGGG 2418
 RESULT 24
 AAD55995
 ID AAD55995 standard; DNA; 5376 BP.
 AC AAD55995;
 XX 07-AUG-2003 (first entry)
 DT
 XX Luciferase gene.
 DE
 XX MxA; GTPase; cancer; gene therapy; cytostatic; luciferase; enzyme; gene;
 KW ds.
 XX Unidentified.
 OS
 XX WO2003033667-A2.
 PN
 XX 24-APR-2003.
 PD
 XX 18-OCT-2002; 2002WO-US033232.
 PF
 XX 18-OCT-2001; 2001US-0329740P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PA Mushinski FJ, Trepel JB, Horisberger MA, Nguyen P, Khanna C;
 PI
 XX WPI; 2003-393519/37.
 DR

XX Use of a polypeptide having at least 90% amino acid sequence identity to
 PT human MxA or a nucleic acid encoding the protein in preparing a
 PT medicament for reducing cancer progression in a mammal.
 XX
 XX Example 7; Page 59-61; 62pp; English.
 XX
 CC The invention relates to the use of a polypeptide having at least 90%
 CC amino acid sequence identity to human MxA or a nucleic acid encoding the
 CC protein. Mx proteins belong to a family of unique GTPases. The invention
 CC is used for preparing a medicament for reducing cancer progression in a
 CC mammal. It is also used in gene therapy. The present sequence is
 CC luciferase gene used in the invention
 CC
 XX Sequence 5376 BP; 1365 A; 1282 C; 1368 G; 1361 T; 0 U; 0 Other;
 SQ
 Query Match 92.4%; Score 19.4; DB 9; Length 5376;
 Best Local Similarity 95.2%; Pred. No. 48;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTCTGTAGTGGGGG 21
 DB 444 GCAAGTCTGCAGGTGGGGG 464
 RESULT 25
 AEB96544
 ID AEB96544 standard; DNA; 49343 BP.
 AC AEB96544;
 XX 06-OCT-2005 (first entry)
 DT
 XX Human MX1 gene, SEQ ID 28.
 DE
 XX hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;
 KW liver cirrhosis; fibrosis; hepatoma; SNP detection; MX1; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH variation 1563
 FT /*tag= a "Single nucleotide polymorphism"
 FT /standard_name= 2802
 FT variation /*tag= b "Single nucleotide polymorphism"
 FT /standard_name= 2869
 FT variation /*tag= c "Single nucleotide polymorphism"
 FT /standard_name= 3159
 FT variation /*tag= d "Single nucleotide polymorphism"
 FT /standard_name= 3836
 FT variation /*tag= e "Single nucleotide polymorphism"
 FT /standard_name= 4105
 FT variation /*tag= f "Single nucleotide polymorphism"
 FT /standard_name= 5232
 FT variation /*tag= g "Single nucleotide polymorphism"
 FT /standard_name= 5251
 FT variation /*tag= h "Single nucleotide polymorphism"
 FT /standard_name= 5558
 FT variation /*tag= i "Single nucleotide polymorphism"
 FT /standard_name= 6034
 FT variation /*tag= j "Single nucleotide polymorphism"
 FT /standard_name= 6135
 FT variation /*tag= k

FT	variation	/standard_name= "Single nucleotide polymorphism"	FT	variation	15487
FT		6684	FT		/tag= aj
FT		/tag= l	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT	variation	15581
FT		7143	FT		/tag= ak
FT		/tag= m	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT	variation	16818
FT		7251	FT		/tag= al
FT		/tag= n	FT		/standard_name= "Single nucleotide polymorphism"
FT		/standard_name= "Single nucleotide polymorphism"	FT	variation	17093
FT	variation	/tag= o	FT		/tag= am
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	9268	FT	variation	17132
FT		/tag= p	FT		/tag= an
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	9392	FT	variation	17151
FT		/tag= q	FT		/tag= ao
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	9544	FT	variation	17190
FT		/tag= r	FT		/tag= ap
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	9596	FT	variation	17278
FT		/tag= s	FT		/tag= aq
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	10001	FT	variation	17794
FT		/tag= t	FT		/tag= ar
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	10206	FT	variation	18284
FT		/tag= u	FT		/tag= as
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	10687	FT	variation	18479
FT		/tag= v	FT		/tag= at
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	11140	FT	variation	18490
FT		/tag= w	FT		/tag= au
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	12204	FT	variation	18624
FT		/tag= x	FT		/tag= av
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	12604	FT	variation	18799
FT		/tag= y	FT		/tag= aw
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	12693	FT	variation	18882
FT		/tag= z	FT		/tag= ax
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	12918	FT	variation	18883
FT		/tag= aa	FT		/tag= ay
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	12936	FT	variation	19506
FT		/tag= ab	FT		/tag= az
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	13584	FT	variation	19582
FT		/tag= ac	FT		/tag= ba
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	13757	FT	variation	20110
FT		/tag= ad	FT		/tag= bb
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	13948	FT	variation	20472
FT		/tag= ae	FT		/tag= bc
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	14111	FT	variation	20947
FT		/tag= af	FT		/tag= bd
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	14200	FT	variation	21968
FT		/tag= ag	FT		/tag= be
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	15242	FT	variation	22058
FT		/tag= ah	FT		/tag= bf
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	15245	FT	variation	22136
FT		/tag= ai	FT		/tag= bg
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT			FT	variation	23330

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FT      /*tag= bh
FT      /standard_name= "Single nucleotide polymorphism"
FT      23384
FT      variation
FT      /*tag= bi
FT      /standard_name= "Single nucleotide polymorphism"
FT      23588
FT      variation
FT      /*tag= bj
FT      /standard_name= "Single nucleotide polymorphism"

Query Match      92.4%; Score 19.4; DB 14; Length 49343;
Best Local Similarity 95.2%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCAAGTGCTGTAGGTGCGGG 21
DB      7098 GCAAGTGCTGCAGGTGCGGG 7118

RESULT 26
ADL92263
ID      ADL92263 standard; DNA; 581 BP.
XX
AC      ADL92263;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #1.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
PF      12-JUL-2002; 2002JP-00204444.
XX
PR      12-JUL-2002; 2002JP-00204444.
XX
PA      (TOKE ) TOSHIBA KK.
XX
PS      WPI; 2004-151026/15.
XX
PT      Detecting target nucleic acid (T) using probe, comprises amplifying
PT      target sequence (S) so that end of (S) which is hybridized with probe is
PT      positioned at less than 40 bases from terminal base of (T) and detecting
PT      hybridization with probe.
XX
PS      Disclosure; SEQ ID NO 20; 47pp; Japanese.
XX
CC      The invention comprises a method for detecting a target nucleic acid. The
CC      method of the invention is useful for: single nucleotide polymorphism
CC      detection, diagnosis of disease by analysing disease-related genes,
CC      estimating risk of incidence of the disease, detection of infection,
CC      analysing virus types, and in toxicity studies. The present nucleic acid
CC      represents a human MxA gene DNA sequence which was used in the
CC      exemplification of the invention.
XX
SQ      Sequence 581 BP; 118 A; 147 C; 213 G; 102 T; 0 U; 1 Other;

Query Match      87.6%; Score 18.4; DB 12; Length 581;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGCTGTAGGTGCGGG 21
DB      410 GCAAGTGCTGNAGGTGCGGG 430

RESULT 27
ADL92265
ID      ADL92265 standard; DNA; 581 BP.
XX
AC      ADL92265;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #3.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
```

```
ADL92266
ID      ADL92266 standard; DNA; 581 BP.
XX
AC      ADL92266;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #4.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
PF      12-JUL-2002; 2002JP-00204444.
XX
PR      12-JUL-2002; 2002JP-00204444.
XX
PA      (TOKE ) TOSHIBA KK.
XX
PS      WPI; 2004-151026/15.
XX
PT      Detecting target nucleic acid (T) using probe, comprises amplifying
PT      target sequence (S) so that end of (S) which is hybridized with probe is
PT      positioned at less than 40 bases from terminal base of (T) and detecting
PT      hybridization with probe.
XX
PS      Disclosure; SEQ ID NO 23; 47pp; Japanese.
XX
CC      The invention comprises a method for detecting a target nucleic acid. The
CC      method of the invention is useful for: single nucleotide polymorphism
CC      detection, diagnosis of disease by analysing disease-related genes,
CC      estimating risk of incidence of the disease, detection of infection,
CC      analysing virus types, and in toxicity studies. The present nucleic acid
CC      represents a human MxA gene DNA sequence which was used in the
CC      exemplification of the invention.
XX
SQ      Sequence 581 BP; 118 A; 149 C; 213 G; 100 T; 0 U; 1 Other;

Query Match      87.6%; Score 18.4; DB 12; Length 581;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGCTGTAGGTGCGGG 21
DB      410 GCAAGTGCTGNAGGTGCGGG 430

RESULT 28
ADL92265
ID      ADL92265 standard; DNA; 581 BP.
XX
AC      ADL92265;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #3.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
```

PF 12-JUL-2002; 2002JP-00204444.

XX 12-JUL-2002; 2002JP-00204444.

XX (TOKE) TOSHIBA KK.

XX WPI; 2004-151026/15.

DR Detecting target nucleic acid (T) using probe, comprises amplifying

XX target sequence (S) so that end of (S) which is hybridized with probe is

PT positioned at less than 40 bases from terminal base of (T) and detecting

PT hybridization with probe.

XX Disclosure; SEQ ID NO 22; 47pp; Japanese.

PS The invention comprises a method for detecting a target nucleic acid. The

XX method of the invention is useful for: single nucleotide polymorphism

CC detection, diagnosis of disease by analysing disease-related genes,

CC estimating risk of incidence of the disease, detection of infection,

CC analysing virus types, and in toxicity studies. The present nucleic acid

CC represents a human MxA gene DNA sequence which was used in the

CC exemplification of the invention.

XX Sequence 581 BP; 120 A; 147 C; 213 G; 100 T; 0 U; 1 Other;

SQ Query Match 87.6%; Score 18.4; DB 12; Length 581;

Best Local Similarity 90.5%; Pred. No. 1.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTTCGGGG 21

|||||

410 GCAAGTGTCTAGGTTCGGGG 430

Db

RESULT 29

ADL92269

ID ADL92269 standard; DNA; 581 BP.

XX ADL92269;

XX 20-MAY-2004 (first entry)

XX Human MxA gene DNA sequence #7.

DE nucleic acid detection; immobilised nucleic acid probe;

XX single nucleotide polymorphism detection; SNP detection;

KW disease diagnosis; ds; human; MxA gene.

KW Homo sapiens.

XX JP2004041109-A.

XX 12-FEB-2004.

XX 12-JUL-2002; 2002JP-00204444.

XX 12-JUL-2002; 2002JP-00204444.

XX (TOKE) TOSHIBA KK.

PA WPI; 2004-151026/15.

XX Detecting target nucleic acid (T) using probe, comprises amplifying

XX target sequence (S) so that end of (S) which is hybridized with probe is

PT positioned at less than 40 bases from terminal base of (T) and detecting

PT hybridization with probe.

XX Disclosure; SEQ ID NO 26; 47pp; Japanese.

PS The invention comprises a method for detecting a target nucleic acid. The

XX method of the invention is useful for: single nucleotide polymorphism

CC detection, diagnosis of disease by analysing disease-related genes,

CC estimating risk of incidence of the disease, detection of infection,

CC analysing virus types, and in toxicity studies. The present nucleic acid

CC represents a human MxA gene DNA sequence which was used in the

XX exemplification of the invention.

XX Sequence 581 BP; 119 A; 147 C; 213 G; 101 T; 0 U; 1 Other;

SQ Query Match 84.8%; Score 17.8; DB 12; Length 581;

Best Local Similarity 90.5%; Pred. No. 2.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTTCGGGG 21

|||||

410 GCAAGTGTCTAGGTTCGGGG 430

Db

RESULT 30

ADL92268

ID ADL92268 standard; DNA; 581 BP.

XX ADL92268;

XX 20-MAY-2004 (first entry)

XX Human MxA gene DNA sequence #6.

XX nucleic acid detection; immobilised nucleic acid probe;

KW single nucleotide polymorphism detection; SNP detection;

KW disease diagnosis; ds; human; MxA gene.

XX Homo sapiens.

XX JP2004041109-A.

XX 12-FEB-2004.

XX 12-JUL-2002; 2002JP-00204444.

XX 12-JUL-2002; 2002JP-00204444.

XX (TOKE) TOSHIBA KK.

XX WPI; 2004-151026/15.

XX Detecting target nucleic acid (T) using probe, comprises amplifying

XX target sequence (S) so that end of (S) which is hybridized with probe is

PT positioned at less than 40 bases from terminal base of (T) and detecting

PT hybridization with probe.

XX Disclosure; SEQ ID NO 25; 47pp; Japanese.

PS The invention comprises a method for detecting a target nucleic acid. The

XX method of the invention is useful for: single nucleotide polymorphism

CC detection, diagnosis of disease by analysing disease-related genes,

CC estimating risk of incidence of the disease, detection of infection,

CC analysing virus types, and in toxicity studies. The present nucleic acid

CC represents a human MxA gene DNA sequence which was used in the

CC exemplification of the invention.

XX Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;

SQ Query Match 84.8%; Score 17.8; DB 12; Length 581;

Best Local Similarity 90.5%; Pred. No. 2.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTTCGGGG 21

|||||

410 GCAAGTGTCTAGGTTCGGGG 430

Db

RESULT 31

ABL34192

ID ABL34192 standard; DNA; 5981 BP.

XX

AC ABL34192;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 2165.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 XX antiarteriosclerotic; aniaemic; cytosine; cytosine; cytosine;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 XX antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 XX ds.
 XX Homo sapiens.
 OS
 XX
 XX WO200200928-A2.
 PN
 XX 03-JAN-2002.
 PD
 XX 02-JUL-2001; 2001WO-EP007537.
 XX
 PF 30-JUN-2000; 2000DE-01032529.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-130909/17.
 DR
 XX Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX
 XX Claim 1; SEQ ID NO 2165; 32pp + Sequence Listing; German.
 PS
 XX The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 CC
 XX Sequence 5981 BP; 1433 A; 174 C; 1715 G; 2659 T; 0 U; 0 Other;
 SQ
 Query Match 84.8%; Score 17.8; DB 6; Length 5981;
 Best Local Similarity 90.5%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTCTGTAGTGGGG 21
 Db 4867 GTAAGTCTGTAGTGGGG 4887
 RESULT 32
 ABL70483
 ID ABL70483 standard; DNA; 5981 BP.
 XX
 XX ABL70483;
 AC
 XX 01-JUL-2002 (first entry)
 DT
 XX Chemically treated cell signalling DNA sequence#187.
 DE
 XX Cell signalling; cytosine methylation; cell signalling disease; cancer;
 KW tumour; cytosine; ds.
 KW
 XX Unidentified.
 OS
 XX

PN WO200202807-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-EP007471.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-154758/20.
 DR
 XX Nucleic acid, useful for diagnosis and therapy of diseases associated
 PT with cell signaling e.g. cancer, comprises chemically modified genomic
 PT sequences of genes associated with cell signaling.
 XX
 XX Claim 1; SEQ ID NO 373; 24pp + Sequence Listing; English.
 PS
 XX The invention relates to a nucleic acid comprising a sequence of at least
 CC 18 bases of a segment of chemically pretreated DNA of genes associated
 CC with cell signalling. The activity of the modified sequences of the
 CC invention may be described as cytostatic. The object of the invention is
 CC to provide the chemically modified DNA of genes associated with cell
 CC signalling, as well as oligonucleotides and/or PNA-oligonucleotides for
 CC detecting cytosine methylations, as well as a method which is
 CC particularly suitable for the diagnosis and/or therapy of genetic and
 CC epigenetic parameters of genes associated with cell signalling. The
 CC chemically modified DNA provided by the invention is useful for diagnosis
 CC and therapy of diseases such as solid tumours and cancer. The sequences
 CC given in records ABL70111-ABL70626 represent chemically pre-treated
 CC genomic DNA's of genes associated with cell signalling. Note: The
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office
 XX
 XX Sequence 5981 BP; 1433 A; 174 C; 1715 G; 2659 T; 0 U; 0 Other;
 SQ
 Query Match 84.8%; Score 17.8; DB 6; Length 5981;
 Best Local Similarity 90.5%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTCTGTAGTGGGG 21
 Db 4867 GTAAGTCTGTAGTGGGG 4887
 RESULT 33
 ABL69125/c
 ID ABL69125 standard; DNA; 3302 BP.
 XX
 XX ABL69125;
 AC
 XX 15-MAY-2002 (first entry)
 DT
 XX Kidney cancer related gene sequence SEQ ID NO:7462.
 DE
 XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytosine; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200194629-A2.
 PN
 XX 13-DEC-2001.
 PD
 XX 30-MAY-2001; 2001WO-US010838.
 XX
 XX 05-JUN-2000; 2000US-0209473P.
 PR

PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 22-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 27-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 PA (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.
 DR Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 7462; 44pp; English.
 XX The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
 CC tumour

SQ Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;
 Query Match 81.0%; Score 17; DB 6; Length 3302;
 Best Local Similarity 100.0%; Pred. No. 5,9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GTGCTGTAGGTGCGGGG 21
 DB 541 GTGCTGTAGGTGCGGGG 525
 RESULT 34
 ADRI4356/c
 ID ADRI4356 standard; DNA; 3302 BP.
 XX
 AC ADRI4356;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human NF-kappaB pathway-associated gene SeqID357.
 XX
 KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Cen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnary; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; gene; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004065577-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 13-JAN-2004; 2004WO-US0000798.
 XX
 PR 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Nadler SG, Neubauer MG, Feder JN, Carman J;
 XX
 DR WPI; 2004-562168/54.
 DR P-PSDB; ADRI4357.
 XX
 PT New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX
 PS Claim 1; SEQ ID NO 357; 237pp; English.
 XX
 CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cyostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Cen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human gene which is
 CC subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX
 XX Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;
 Query Match 81.0%; Score 17; DB 13; Length 3302;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGG 21
 |||||
 Db 541 GTGCTGTAGTGGGG 525

RESULT 35
 ADX07310/c
 ID ADX07310 standard; DNA; 3302 BP.
 AC ADX07310;
 XX
 XX 21-APR-2005 (first entry)
 DT
 XX
 XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1875.
 DE
 XX
 XX cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.

XX Homo sapiens.
 OS
 XX WO2005012875-A2.
 PN
 XX
 XX 10-FEB-2005.
 PD
 XX
 XX 29-JUL-2004; 2004WO-US024424.
 PF
 XX
 XX 29-JUL-2003; 2003US-0490890P.
 PR
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX
 XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 PI
 XX P-PSDB; ADX07311.
 DR
 XX
 XX WPI; 2005-163068/17.

PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.

XX Claim 5; SEQ ID NO 1875; 141pp; English.
 XX
 CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO.1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for

CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
 CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
 CC sequence encodes a biomarker used in the method of the invention.

XX
 XX Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;
 Query Match 81.0%; Score 17; DB 14; Length 3302;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGG 21
 |||||
 Db 541 GTGCTGTAGTGGGG 525

RESULT 36
 ADZ49006/c
 ID ADZ49006 standard; DNA; 3302 BP.
 AC ADZ49006;
 XX
 XX 30-JUN-2005 (first entry)
 DT
 XX
 XX Insulin signaling pathway related gene, SEQ ID 335.
 DE
 XX
 XX Antidiabetic; Gene Therapy; Non-insulin dependent diabetes;
 KW
 KW insulin resistance; gene; ds.

XX Homo sapiens.
 OS
 XX US2005085436-A1.
 FN
 XX
 XX 21-APR-2005.
 PD
 XX
 XX 08-JUL-2004; 2004US-00887553.
 PF
 XX
 XX 08-JUL-2003; 2003US-0485883P.
 PR
 XX
 XX (LIHH/) LI H.
 PA (MAJJ/) MA J.
 PA
 XX
 XX Li H, Ma J;
 PI
 XX WPI; 2005-305194/31.

DR Treating, preventing or ameliorating pathological conditions associated
 XX with dysregulation of the insulin signaling pathway (ISP) comprises
 XX administering to a subject an amount of a modulator of any of the
 XX proteins regulated by ISP.

XX Disclosure; SEQ ID NO 335; 70pp; English.
 XX
 XX The present invention relates to a method for treating, preventing or
 XX ameliorating pathological conditions associated with dysregulation of the
 XX insulin signaling pathway (ISP). The method comprises administering to a
 XX subject a modulator for ISP-regulated proteins or a pharmaceutical
 XX composition comprising the described modulator. The method is useful for
 XX treating, preventing or ameliorating pathological conditions associated
 XX with dysregulation of the ISP such as Type II diabetes or Type A syndrome
 XX of insulin resistance. The present sequence is a human homolog of a
 XX Drosophila gene regulated by ISP. Note: The sequence data for this patent
 XX did not form part of the printed specification, but was obtained in
 XX electronic format directly from USPTO at
 XX seqdata.uspto.gov/sequence.html?docID=20050085436.
 XX
 XX Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;

```
Query Match      81.0%; Score 17; DB 14; Length 3302;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
DB 541 GTGCTGTAGTGGCGGG 525

RESULT 37
ACN90319/c
ID AEB56452 standard; cDNA; 3302 BP.
XX
AC AEB56452;
XX
XX 20-OCT-2005 (first entry)
XX
DE Radiochemotherapy response detection associated cDNA SEQ ID NO 27.
XX
XX gene expression; chemotherapy; radiotherapy; prognosis; diagnosis;
KW adenocarcinoma; cytostatic; neoplasm; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2005073411-A1.
PN
XX 11-AUG-2005.
PD
XX 12-JAN-2005; 2005WO-US000891.
PF
XX 12-JAN-2004; 2004US-0535491P.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Ried T, Difilippantonio MJ, Ghadimi B, Grade M, Becker H;
PI Liersch T;
XX
XX WPI; 2005-555710/56.
DR
XX P-PSDB; AEB56509.
DR
XX New compositions having isolated nucleic acids, polypeptides and
PT antibodies, useful for diagnosing, detecting radiochemotherapy response
PT and prognosticating rectal adenocarcinomas.
PT
XX Claim 16; SEQ ID NO 27; 266pp; English.
PS
XX The invention describes a composition comprising at least 5 isolated
CC nucleic acids of at least 15 contiguous nucleotides selected from nucleic
CC acids that correspond to genes 1-54 from any of 54 significantly changed
CC genes in class comparison analysis, given in the specification as Table
CC 3, and comprising no more than 9000 total isolated nucleic acids. The
CC methods and compositions of the present invention are useful for
CC diagnostic and research applications, in particular for diagnosing,
CC detecting radiochemotherapy response and prognosticating rectal
CC adenocarcinomas. This sequence represents a cDNA the expression of which
CC is altered in rectal adenocarcinoma cells.
XX
SQ Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;

Query Match      81.0%; Score 17; DB 14; Length 3302;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
DB 541 GTGCTGTAGTGGCGGG 525

RESULT 38
ACN90319/c
ID ACN90319 standard; DNA; 3579 BP.
XX
```

```
AC ACN90319;
XX
DT 02-DEC-2004 (first entry)
XX
DE Breast cancer related marker, seq id 11469.
XX
KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS Homo sapiens.
XX
XX US2003099974-A1.
PN
XX 29-MAY-2003.
PD
XX 18-JUL-2002; 2002US-00198846.
PF
XX 18-JUL-2001; 2001US-0306220P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI
XX WPI; 2003-787014/74.
DR
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
PT
XX Disclosure; SEQ ID NO 11469; 36pp; English.
PS
XX The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
XX
SQ Sequence 3579 BP; 900 A; 929 C; 867 G; 862 T; 0 U; 21 Other;

Query Match      81.0%; Score 17; DB 11; Length 3579;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
DB 628 GTGCTGTAGTGGCGGG 612

RESULT 39
ACF74962
ID ACF74962 standard; DNA; 633 BP.
XX
XX ACF74962;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX Staphylococcus aureus DNA #2642.
DE
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target; gene; ds.
KW
XX Staphylococcus aureus.
OS
XX WO200294868-A2.
PN
XX 28-NOV-2002.
PD
XX
```

PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001CB-00007661.
XX
PA (CHTR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
XX
DR P-PSDB; ABW73402.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
PS Claim 6; SEQ ID NO 5283; 49pp; English.
XX
CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus genes of the invention
XX
SQ Sequence 633 BP; 183 A; 97 C; 132 G; 221 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 8; Length 633;
Best Local Similarity 90.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGTGTGGG 20
Db 457 GCAAGTTATGTAGTGTGGG 476
RESULT 40
AAS93751/c
ID AAS93751 standard; cDNA; 954 BP.
XX
AC AAS93751;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #29555.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG29564.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess

PT biodiversity.
XX
PS Claim 1; SEQ ID NO 29555; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application of mutations
CC in diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 954 BP; 215 A; 283 C; 267 G; 189 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 5; Length 954;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGTGTGGG 20
Db 210 GTAACTGCTGTAGTGTGGG 191
RESULT 41
AAS81868/c
ID AAS81868 standard; cDNA; 1840 BP.
XX
AC AAS81868;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #17672.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG17681.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 1; SEQ ID NO 17672; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1840 BP; 413 A; 513 C; 525 G; 389 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 5; Length 1840;

Best Local Similarity 90.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20

DB 210 GTAAGTGTCTAGGTGCGGG 191

RESULT 42

AAD01353/c

ID AAD01353 standard; cDNA; 1972 BP.

XX

AC AAD01353;

XX

DT 12-OCT-2000 (first entry)

XX

DE Wheat sphingolipid desaturase cDNA #1.

XX

KW Wheat; sphingolipid desaturase; membrane-bound desaturase;

KW transgenic plant; fatty acid; ss.

XX

OS Triticum aestivum.

XX

FH Key Location/Qualifiers

FT CDS 124..1533

FT /*tag= a

FT /product= "sphingolipid desaturase"

XX

PN WO200032790-A2.

XX

PD 08-JUN-2000.

XX

PF 02-DEC-1999; 99WO-US028589.

XX

PR 03-DEC-1998; 98US-0110784P.

XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX

PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX

DR WPI; 2000-412336/35.

DR P-PSDB; AAY71555.

XX

PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing

PT transgenic plants and for producing antibodies specific to which is

PT useful for screening cDNA expression libraries.

XX

PS Disclosure; Page 48-49; 57pp; English.

XX The present sequence is a cDNA encoding sphingolipid desaturase from

CC clone wrel.pk0004.c7.fis isolated from wheat etiolated seedling root cDNA

CC library, wrel. The present sequence is useful for producing transgenic

CC plants having altered levels of sphingolipid desaturase which in turn

CC would alter the fatty acid composition. The enzyme is useful for

CC producing polyclonal or monoclonal antibodies. The polynucleotide is also

CC useful as primer or probe for screening cDNA libraries to isolate desired

CC full-length cDNA clones

XX

SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 3; Length 1972;

Best Local Similarity 90.0%; Pred. No. 7.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20

DB 829 GCAAGTGTCTAGGTGCGGG 810

RESULT 43

AAS81864/c

ID AAS81864 standard; cDNA; 2178 BP.

XX

AC AAS81864;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #17668.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG17677.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX

PS Claim 1; SEQ ID NO 17668; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2178 BP; 481 A; 626 C; 632 G; 439 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 5; Length 2178;
Best Local Similarity 90.0%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGGTGCGGG 20
Db 1623 GTAACGTCTAGGTGCGGG 1604
RESULT 44
AAS89697/c
ID AAS89697 standard; cDNA; 2179 BP.
XX
AC AAS89697;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #25501.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
WPI; 2001-639362/73.
DR P-PSDB; ABG25510.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 25501; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2179 BP; 481 A; 627 C; 632 G; 439 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 5; Length 2179;
Best Local Similarity 90.0%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGGTGCGGG 20
Db 1623 GTAACGTCTAGGTGCGGG 1604
RESULT 45
AAS93754/c
ID AAS93754 standard; cDNA; 2250 BP.
XX
AC AAS93754;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #29558.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
WPI; 2001-639362/73.
DR P-PSDB; ABG29567.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 29558; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2250 BP; 505 A; 615 C; 628 G; 502 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 5; Length 2250;
Best Local Similarity 90.0%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGTGGCGG 20
DB 663 GTAAGTGTCTAGTGGCGG 644
RESULT 46
AAS93758/c
ID AAS93758 standard; cDNA; 2830 BP.
XX
AC AAS93758;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #29562.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR P-PSDB; ABG29571.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 29562; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2830 BP; 599 A; 761 C; 884 G; 586 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 5; Length 2830;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTGTCTAGTGGCGG 20
DB 1965 GTAAGTGTCTAGTGGCGG 1946
RESULT 47
AAS93339/c
ID AAS93339 standard; cDNA; 3039 BP.
XX
AC AAS93339;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #29143.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR P-PSDB; ABG29152.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 29143; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 3039 BP; 658 A; 790 C; 883 G; 708 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16.8; DB 5; Length 3039;
 Best Local Similarity 90.0%; Pred. No. 7.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTGTCTAGGTGCGGG 20
 |||||
 Db 2829 GTAACGTCTAGGTGCGGG 2810
 RESULT 48
 AAS89661/C
 ID AAS89661 standard; cDNA; 3039 BP.
 AC AAS89661;
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #25465.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US008631.
 PF 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR P-PSDB; ABG25474.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 1; SEQ ID NO 25465; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS84197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 3039 BP; 658 A; 790 C; 883 G; 708 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16.8; DB 5; Length 3039;
 Best Local Similarity 90.0%; Pred. No. 7.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTGTCTAGGTGCGGG 20
 |||||
 Db 2829 GTAACGTCTAGGTGCGGG 2810
 RESULT 49
 AAS93240
 ID AAS93240 standard; cDNA; 3039 BP.
 AC AAS93240;
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #29044.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US008631.
 PF 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR P-PSDB; ABG29053.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 1; SEQ ID NO 29044; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 3039 BP; 708 A; 883 C; 790 G; 658 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 5; Length 3039;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTAGTGGGG 20
Db 211 GTAACGTCTAGTGGGG 230

RESULT 50

AAS85756
ID AAS85756 standard; cDNA; 3355 BP.

XX AC AAS85756;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #21560.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG21569.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX PS Claim 1; SEQ ID NO 21560; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (II) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 3355 BP; 714 A; 964 C; 897 G; 780 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 5; Length 3355;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTAGTGGGG 20

Db 457 GTAACGTCTAGTGGGG 476

Search completed: January 27, 2006, 05:44:40
Job time : 222.5 secs

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